



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 1642-002

**TO:** Catherine Joyce  
**Location:** REM/4C04/3C18  
**Art Unit:** 1642  
**Tuesday, October 04, 2005**

**Case Serial Number:** 10/645094

**From:** Edward Hart  
**Location:** Biotech-Chem Library  
**REM-1A55**  
**Phone:** 571-272-2512

**edward.hart@uspto.gov**

### Search Notes

Examiner Joyce,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

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169604

From: Joyce, Catherine  
Sent: Monday, October 03, 2005 4:11 PM  
To: STIC-Biotech/ChemLib  
Subject: 10/645094

Please search the following sequences:

SEQ ID NO:1 (polypeptide)

Catherine Joyce  
Art Unit 1642  
Ph. 571-272-3321  
Office: 4C04  
Mailbox: 3C18

RECEIVED  
OCT -4 2005  
SEARCHED, INDEXED  
(STIC)

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: *10/4/05*  
Date completed: *10/7/05*  
Searcher Prep Time: *10/4/05*  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search /  
NA# \_\_\_\_\_ AA#: \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: *DDP*  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

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## **Protein Sequence Searches - February 2005**

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

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Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches. Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions .rnpn and .rnppn. Searches run against the Amino Acid Pending database produce two sets of results, with the extensions .rapm and .rapn.

***Because they contain data that is confidential, the results of Pending database searches should not be left in the case.***

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# STIC SEARCH RESULTS FEEDBACK FORM

## Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact:*

Mary Hale, Information Branch Supervisor  
Remsen Bldg. 01 D86  
571-272-2507

## Voluntary Results Feedback Form

- I am an examiner in Workgroup:  Example: 1610
- Relevant prior art found, search results used as follows:
- 102 rejection
  - 103 rejection
  - Cited as being of interest.
  - Helped examiner better understand the invention.
  - Helped examiner better understand the state of the art in their technology.

*Types of relevant prior art found:*

- Foreign Patent(s)
- Non-Patent Literature  
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art not found:

- Results verified the lack of relevant prior art (helped determine patentability).
- Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC Biotech-Chem Library, Remsen Bldg.



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OM protein - protein search, using sw model						
Run on: October 4, 2005, 13:46:40 ; Search time 180 Seconds (without alignments) 1490.719 Million cell updates/sec						
Title:	US-10-645-094-1					
Perfect score:	2703					
Sequence:	1 MNHUVVKRLSVSVLITV.....TNINKVANESTIEHTKDEL 524					
Scoring table:	BLOSUM62					
Gapop table:	Gapop 10.0 , Gapext 0.5					
Searched:	1612378 seqs, 512079187 residues					
Total number of hits satisfying chosen parameters:	1612378					
Minimum DB seq length:	0					
Maximum DB seq length:	2000000000					
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries					
Database :	Uniprot 03 : * 2: uniprot_sprefit: 2: uniprot_trembl: *					
SUMMARIES						
Result No.	Score	Query Match Length	DB ID	Description		
1	2699	99. 9	524	Q9IBA7	Q9IBA7 scomber japonicus	
2	1156.5	42. 8	523	Q8VBN4	Q8VBN4 mus musculus	
3	1096.5	40. 6	504	Q90w54	Q90w54 agkistrodon	
4	1089.5	40. 3	504	Q6STF1	Q6STF1 agkistrodon	
5	1079.5	39. 9	516	QXLA_AGKRH	QXLA_AGKRH	
6	1063.5	39. 3	516	Q9PWQ9	Q9PWQ9 crotalus adamanteus	
7	1059.5	39. 2	497	Q6TGQ9	Q6TGQ9 bothrops jararaca	
8	1059.5	39. 2	516	QXLA_CROAD	QXLA_CROAD	
9	1058.5	39. 2	478	Q6TGQ8	Q6TGQ8 bothrops矛頭蝮	
10	1055.0	39. 0	516	Q6WP39	Q6WP39 trimetresurus	
11	1052.5	38. 9	516	Q7T062	Q7T062 trimetresurus	
12	1048.5	38. 9	523	Q9JJK6	Q9JJK6 mus musculus	
13	1034	38. 3	630	Q1G1_MOUSE	Q1G1_MOUSE	
14	1034	38. 3	630	Q6YBV6	Q6YBV6 mus musculus	
15	1034	38. 3	630	Q6YD18	Q6YD18 mus musculus	
16	1030	38. 1	630	Q6Y632	Q6Y632 mus musculus	
17	999	37. 0	567	FIG1_HUMAN	Q9ZCQ9 homo sapiens	
18	999	37. 0	588	Q8Tams5	Q8Tams5 homo sapiens	
19	999	37. 0	588	Q6P203	Q6P203 homo sapiens	
20	823.5	30. 5	490	Q739P2	Q739P2 bacillus amyloliquefaciens	
21	818.5	30. 3	482	Q8IEG3	Q8IEG3 bacillus ceulensis	
22	818.5	30. 3	485	Q31334	Q31334 bacillus ceulensis	
23	817.5	30. 2	478	Q8IRW3	Q8IRW3 bacillus amyloliquefaciens	
24	812.5	30. 1	485	Q6HJU8	Q6HJU8 bacillus ceulensis	
25	807.5	29. 9	482	Q63CE2	Q63CE2 bacillus ceulensis	
26	807.5	29. 9	482	Q8IRM4	Q8IRM4 bacillus amyloliquefaciens	
27	796.5	29. 5	478	Q739X9	Q739X9 bacillus ceulensis	
28	777.5	28. 8	478	Q63CN0	Q63CN0 bacillus ceulensis	
29	773.5	28. 6	478	Q6HK30	Q6HK30 bacillus thuringiensis	
30	761.5	28. 2	478	Q8Lep3	Q8Lep3 bacillus ceulensis	
31	751	27. 8	509	Q8R2q8	Q8R2q8 mus musculus	

32	737.5	27.3	446	2	Q34363	bacillus su
33	711.5	26.3	485	2	Q8BRK6	oceanobacillus
34	642	23.8	709	2	Q9AIT1	streptomyces
35	641	23.7	701	2	QBLJC7	streptomyces
36	591	21.9	309	2	Q9CUM6	mus muscu
37	489	18.1	332	2	Q65JJD2	bacillus li
38	421	15.6	473	2	Q8KH50	noicardia ae
39	412	15.2	526	2	Q9RYN6	deinococcus
40	411	15.2	527	2	Q8P5Q8	xanthomonas
41	403	14.9	527	2	Q8PH34	xanthomonas
42	399.5	14.8	696	1	QXLA_NEUCR	p23623 neurospora
43	396.5	14.7	504	2	Q83WQ4	streptomyces
44	392	14.5	426	2	Q8YK99	anabaena sp
45	383.5	14.2	541	2	Q9A4N7	caulobacter
RESULT 1						
Q918A7	ID	Q918A7	PRELIMINARY;	PRT;	524 AA.	
AC	Q918A7;					
DT	01-OCT-2000	(TREMBLrel.	15,	Created)		
DT	01-OCT-2000	(TREMBLrel.	15,	Last sequence update)		
DT	01-MAR-2004	(TREMBLrel.	26,	Last annotation update)		
DE	Endoplasmic reticulum luminal L-amino acid oxidase precursor.					
GN	Name=lao;					
OS	Scomber japonicus	(Chub mackerel)				
OC	Actinopterygii;	Chordata;	Cyprinidae;	Vertebrata;	Euteleostomi;	
OC	Actinopterygii;	Neopterygii;	Tetraodontiformes;	Buteleosteoi;	Neoteleosteoi;	
OC	Acanthopercygii;					
SC	Scombridae;	Scomber;				
NCBI_TAXID=13676;						
[1]						
RN	SEQUENCE FROM N.A.					
RX	MedlineID=20363838; PubMed=10903755;					
RA	Jung S. K., Mai A., Iwamoto M., Arizono N., Fujimoto D., Sakamaki K.,					
RA	Yonehara S.;					
RT	"Purification and cloning of an apoptosis-inducing protein derived from fish infected with Anisakis simplex, a causative nematode of human anisakiasis."					
RT	J. Immunol. 165:1491-1497 (2000).					
RL	Embl: AJ400871; CAC00499.1; -.					
DR	GO; GO:0006118; P:electron transport; IBA.					
DR	GO; GO:0016191; P:oxidoreductase activity; IBA.					
DR	HSSP; P81382; 1FB85.					
DR	InterPro; IPR00759; Ahrndx_reductase.					
DR	InterPro; IPR01613; Amineoxid_f1.					
DR	InterPro; IPR02937; Amino_oxidase.					
DR	InterPro; IPR00886; ER_target_S.					
DR	InterPro; IPR00205; NAD_BS.					
DR	Pfam: PF01533; Amino oxidase.					
DR	PRINTS; PR00419; ADXRDASE.					
DR	PRINTS; PR00757; AMINEOXDASEF.					
DR	PROSITE; PS00014; ER_TARGET; UNKNOWN_1.					
KW	Signal.	1	30	Potential endoplasmic reticulum luminal L-amino acid oxidase.		
FT	CHAIN	31	524	58623 NW; 5C17ACA07E74397E CRC64;		
FT	SEQUENCE	524 AA;				
Query	Match	99.9%	Score 2699;	DB 2;	Length 524;	
Best	Local Similarity	99.8%	Pred. No. 1.6e-158;			
Matches	523;	Conservative	1; Mismatches 0;	Indels 0;	Gaps 0	
Qy	1	MNLHVWKRKLSSVSLVLTLYSHTYVALSKELHADCLEDKYDTLQLTLDLGHLPHINTSH	60			
Db	1	MNLHVWKRKLSSVSLVLTLYSHTYVALSKELHADCLEDKYDTLQLTLDLGHLPHINTSH	60			
Qy	61	HVYIVGAGMAGLTAAKJLQDAGHTTILEANDRIGCRVETYRNKEKGWYAENGAMR_PSS	120			
Db	61	HVYIVGAGMAGLTAAKJLQDAGHTTILEANDRIGCRVETYRNKEKGWYAENGAMR_PSS	120			

Qy	121 HRIVQFWVKLGVMENFVMTDDNTPYLVLNGYRERTYVQENPDVLYKVNYESESEKGKISSAD 180	DR HSSP; P813B2; 1FOR.
Db	121 HRIVQFWVKLGVMENFVMTDDNTPYLVLNGYRERTYVQENPDVLYKVNYESESEKGKISSAD 180	DR MGD; MG1:2140628; Lao1.
Qy	181 DLDRLQKVKEEVEANGKALEYKDYSKEYLKEGGISPGAVRMICDLNEQSILMY 240	DR GO; GO:0005615; C:extracellular space; TAS.
Db	181 DLDRLQKVKEEVEANGKALEYKDYSKEYLKEGGISPGAVRMICDLNEQSILMY 240	DR GO; GO:0001716; F:L-amino-acid oxidase activity; IDA.
Qy	241 TALESMYDQADYNDSYTYHETGGSDLPEAFLSVLDVPIIANSKVKHTRQSDKGVIVS 300	DR GO; GO:0009063; P:amino acid catabolism; IDA.
Db	241 TALESMYDQADYNDSYTYHETGGSDLPEAFLSVLDVPIIANSKVKHTRQSDKGVIVS 300	DR P00419; Amino oxidase; 1.
Qy	301 YOTGNESSESLMDLSADIYLTTAKAALFIDFAPPSTSKEMLRSYHDSTSSTKILLTFRD 360	DR PRINTS; PR00757; AMINOXIDASE.
Db	301 YOTGNESSESLMDLSADIYLTTAKAALFIDFAPPSTSKEMLRSYHDSTSSTKILLTFRD 360	DR PRINTS; PR00370; FMOXYGENASE.
Qy	361 KEWBDGGRGGSITDGESRYIYPHSFHNETIGVLLASYTWSDESLFLGASDEELK 420	DR SQ SEQUENCE 523 AA; P631592D7117AOB CRC64;
Db	361 KEWBDGGRGGSITDGESRYIYPHSFHNETIGVLLASYTWSDESLFLGASDEELK 420	Query Match Score 1156.5; DB 2; Length 523;
Qy	421 ELALRDIAKTHGEQWWDCTGIVKVKRWAQPSLGAFAFLPYQHLEYAQELFSSEGRVH 480	Best Local Similarity 47.1%; Pred. No. 3.6e-63;
Db	421 ELALRDIAKTHGEQWWDCTGIVKVKRWAQPSLGAFAFLPYQHLEYAQELFSSEGRVH 480	Matches 235; Conservative 85; Mismatches 172; Indels 7; Gaps 4;
Qy	481 FAGEHTAFAPHAWIETSMKSAIRATINNKVANEESTIHKDEL 524	Query 27 LSLEKHADCLEDKDYLQLDNLPHINTSHHVVVYVGAGMAGTAALKLIQDAGHRTV 86
Db	481 FAGEHTAFAPHAWIETSMKSAIRATINNKVANEESTIHKDEL 524	Query 25 LALYENLVRFCQDDYEAFLLIAQNLGHSTSPLSKRVRVVGAGNAGLVAAKTLDQAGHETV 84
Qy	523 AA.	Query 87 ILEANDRVGRVETYVNRNEKEGIVWAEAMGARIPSSHIVQWVFKLGVMEMEFYMDNDTF 146
Db	PRT; 523 AA;	Query 85 ILEASHNHIGGRVYTILRKKEEGWYLEGPMPRIPESHKLHTYVQGLGLKLNKFNOYDSNTW 144
Qy	PRT; 523 AA.	Query 147 YLVNGCVRERTYVVDENPDVLYKVNSESEKGISADDLLDALQKVKEEVBANGKALEY 206
Db	PRT; 523 AA.	Query 145 YLLNGQYRASEVMANPGILGYPPRSEKNTVTDLFYQAITKPKHRTTSNCQLLIS 204
Qy	PRT; 523 AA.	Query 207 DRYSKYKEYLKEEGGSPGAVRMIGDILNEQSLMTALSIMYDADYNDSVTVEVTGES 266
Db	PRT; 523 AA.	Query 205 DSYSKAYLMKEGTISKGAIEMICDMMENAGYKSLLESLRITASFSKSQDFSEITGGF 264
Qy	PRT; 523 AA.	Query 267 DLLPFAF-LSVLDPVILLASKVKHTRQSDKGVIVSQT-GNESSIMLDSADIVLVTTPAK 324
Db	PRT; 523 AA.	Query 265 DQLPGLSASLKPCTIRLGSKVERVVRDGPVKVNMRTDGTSAHLKUTADYAITASAK 324
Qy	PRT; 523 AA.	Query 325 AALFDIDFPPLUSIMKMEARSVHYDSSSTKLLTPRDKEMDGIGRKGSITDGPSPRYIXY 384
Db	PRT; 523 AA.	Query 325 ATRLTFQPPLSRECTHALRSVHYTSATKVLVCNERFEQDGTRGGYSITDPRSRFTY 384
Qy	PRT; 523 AA.	Query 385 PSHSHTNETIGVLLASYTWSDESLFLGASDEBKELALDIAKTH--GEQWWDCTG 441
Db	PRT; 523 AA.	Query 385 PSHSHPGGK-GVLLASFTVGDSSFFAAALKPNQUDVVLDDLAAVHRIPEKELKRMCPK 442
Qy	PRT; 523 AA.	Query 442 VIKKWSADPYSLGAFALFTPYQHLEYAQELFSSEGRVHFAGENTAFPHAWIETSMKSAI 501
Db	PRT; 523 AA.	Query 443 SAIKWSLDPTTIGAFTEFTPYQFVDSYKSLSQPPGRYFAGENHCLPWSWIDRIKSGI 502
Qy	PRT; 523 AA.	RESULT 3 Q90W54 PRELIMINARY; PRT; 504 AA.
Db	PRT; 523 AA.	RESULT 3 Q90W54 PRELIMINARY; PRT; 504 AA.
AC	QBVEN4 PRELIMINARY,	ID Q90W54 PRELIMINARY; PRT; 504 AA.
ID	QBVEN4 PRELIMINARY,	ID Q90W54 PRELIMINARY; PRT; 504 AA.
DT	01-MAR-2002 (TREMBLrel. 20, Created)	ID Q90W54 PRELIMINARY; PRT; 504 AA.
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)	ID Q90W54 PRELIMINARY; PRT; 504 AA.
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)	ID Q90W54 PRELIMINARY; PRT; 504 AA.
DE	L-amino acid oxidase 1.	ID Q90W54 PRELIMINARY; PRT; 504 AA.
GN	Name=Lao1;	ID Q90W54 PRELIMINARY; PRT; 504 AA.
OS	Mus musculus (Mouse).	ID Q90W54 PRELIMINARY; PRT; 504 AA.
OC	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	ID Q90W54 PRELIMINARY; PRT; 504 AA.
OC	Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.	ID Q90W54 PRELIMINARY; PRT; 504 AA.
NCBI_TaxID	10090;	ID Q90W54 PRELIMINARY; PRT; 504 AA.
RN	[1]	ID Q90W54 PRELIMINARY; PRT; 504 AA.
RP	SEQUENCE FROM N.A.	ID Q90W54 PRELIMINARY; PRT; 504 AA.
RC	STRAIN=FVB/N, TISSUE= Mammary tumor;	ID Q90W54 PRELIMINARY; PRT; 504 AA.
RX	MEDLINE=22388457; PubMed=1247933; DOI=10.1073/pnas.242603899;	ID Q90W54 PRELIMINARY; PRT; 504 AA.
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	ID Q90W54 PRELIMINARY; PRT; 504 AA.
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	ID Q90W54 PRELIMINARY; PRT; 504 AA.
RA	Altshull S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,	ID Q90W54 PRELIMINARY; PRT; 504 AA.
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	ID Q90W54 PRELIMINARY; PRT; 504 AA.
RA	Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	ID Q90W54 PRELIMINARY; PRT; 504 AA.
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	ID Q90W54 PRELIMINARY; PRT; 504 AA.
RA	Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Oranje C.,	ID Q90W54 PRELIMINARY; PRT; 504 AA.
RA	Raha S.S., Loguello N.A., Peters G.J., Abramson R.D., Mullally S.J.,	ID Q90W54 PRELIMINARY; PRT; 504 AA.
RA	Bosbach S.A., McElwain P.J.C., McKernan K.J., Malek J.A., Gunaratne P.H.,	ID Q90W54 PRELIMINARY; PRT; 504 AA.
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	ID Q90W54 PRELIMINARY; PRT; 504 AA.
RA	Villalon D.K., Muzy N.D.M., Sodergren E.J., Lu X., Gibbs R.A.,	ID Q90W54 PRELIMINARY; PRT; 504 AA.
RA	Fahney J., Helton E., Kettman M.M., Madan A., Rodriguez S., Sanchez A.,	ID Q90W54 PRELIMINARY; PRT; 504 AA.
RA	Whiting M., Madan A., Young A.C., Shevchenko A., Boutard G.G.,	ID Q90W54 PRELIMINARY; PRT; 504 AA.
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	ID Q90W54 PRELIMINARY; PRT; 504 AA.
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,	ID Q90W54 PRELIMINARY; PRT; 504 AA.
RA	Krzywinski M.I., Smaltska U., Smalts D.E., Schein J.E.,	ID Q90W54 PRELIMINARY; PRT; 504 AA.
RA	Jones S.J., Marrs M.A.; Generation and initial analysis of more than 15,000 full-length human	ID Q90W54 PRELIMINARY; PRT; 504 AA.
RA	and mouse cDNA sequences,"	ID Q90W54 PRELIMINARY; PRT; 504 AA.
RA	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	ID Q90W54 PRELIMINARY; PRT; 504 AA.
RA	[2]	ID Q90W54 PRELIMINARY; PRT; 504 AA.
RA	SEQUENCE FROM N.A.	ID Q90W54 PRELIMINARY; PRT; 504 AA.
RC	STRAIN=FVB/N, TISSUE= Mammary tumor;	ID Q90W54 PRELIMINARY; PRT; 504 AA.
RA	Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.	ID Q90W54 PRELIMINARY; PRT; 504 AA.
DR	EMBL; BC017599; AAH17599.1; -.	ID Q90W54 PRELIMINARY; PRT; 504 AA.
RA	Takatsuka H., Sakurai Y., Yoshioka A., Kokubo T., Usami Y., Suzuki M., Matsui T., Titani K., Yagi H., Matsumoto M., Fujimura Y.;	ID Q90W54 PRELIMINARY; PRT; 504 AA.
RA	"Molecular characterization of L-amino acid oxidase from Agkistrodon halsys blomhoffii with special reference to platelet aggregation."	ID Q90W54 PRELIMINARY; PRT; 504 AA.

RL	Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AB072392; BA069450.1; -.
DR	PDB; 1TDX; X-ray; A=.
DR	PDB; 1TDO; X-ray; A=.
DR	GO; GO:0001716; F: L-amino-acid oxidase activity; IEA.
DR	GO; GO:0016491; F: oxidoreductase activity; IEA.
DR	GO; GO:0006118; Peletor transport; IEA.
DR	InterPro; IPR002837; Amino oxidase.
DR	InterPro; IPR000505; NAD <sup>+</sup> Ba.
DR	Pfam; PF01533; Amino oxidase; 1.
DR	KW Oxidoreductase; Signal.
FT SIGNAL_1 18	Potential.
SEQUENCE 504 AA;	57091 MW; 17F57B46E646F12A CRC64;
Query Match 40.6%; Score 1096.5; DB 2; Length 504;	
Best Local Similarity 44.4%; Pred. No. 1..e-59;	
Matches 215; Conservative 96; Mismatches 166; Indels 7; Gaps 4;	
Qy 33 LADCLEDKDYDTLQLTDLGLPHINTSHVIVAGMAGLTAALKLQDAGHTVTLAND 92	Qy 33 LADCLEDKDYDTLQLTDLGLPHINTSHVIVAGMAGLTAALKLQDAGHTVTLAND 92
Db 25 LEECFRETDYEEFLERANGLKLATSNPKHIVVINGAGMSGLSAYVLSAGHQTVEASE 84	Db 25 LEECFRETDYEEFLERANGLKLATSNPKHIVVINGAGMSGLSAYVLSAGHQTVEASE 84
Qy 93 RVGGRVETYRNEKEGWAEMGAMRIPSSHRIVQWFVKLGVENNEFYMTDDNTFYLNGV 152	Qy 93 RVGGRVETYRNEKEGWAEMGAMRIPSSHRIVQWFVKLGVENNEFYMTDDNTFYLNGV 152
Db 85 RAGGRVRYRNDKEDWYANLGPMRLPEGRVIREYIRKGLQLINEFSQENDNAWYFKNI 144	Db 85 RAGGRVRYRNDKEDWYANLGPMRLPEGRVIREYIRKGLQLINEFSQENDNAWYFKNI 144
Qy 153 RERTYYQQENPDVLYKVNSESEGKISADDLDRALQKVKEEVAANGKAALEKYDRYSVK 212	Qy 153 RERTYYQQENPDVLYKVNSESEGKISADDLDRALQKVKEEVAANGKAALEKYDRYSVK 212
Db 145 RKGVEGEVKDPGVLKYPKPKPSEGKSAGOLYEBLSGKVEELKRTNCSYILNKYDTSTK 204	Db 145 RKGVEGEVKDPGVLKYPKPKPSEGKSAGOLYEBLSGKVEELKRTNCSYILNKYDTSTK 204
Qy 213 EYLKEEGGLSPGAVRMIGDLNLNEQSLMYTALEMISYIYDQADVNDSVTYHEVTGGSDLPLEA 272	Qy 213 EYLKEEGGLSPGAVRMIGDLNLNEQSLMYTALEMISYIYDQADVNDSVTYHEVTGGSDLPLEA 272
Db 205 EYLKEGNLSPGAVIDMGDLNEDSYIVSFPSPLRHDIDFAYEKRPFBIVGMDKLPDS 264	Db 205 EYLKEGNLSPGAVIDMGDLNEDSYIVSFPSPLRHDIDFAYEKRPFBIVGMDKLPDS 264
Qy 273 FLSVLVDVPILLNSKVKHTRQSKDGVIVSYQTGNESLMLSDASDIVLVTTAKAALFIDFD 332	Qy 273 FLSVLVDVPILLNSKVKHTRQSKDGVIVSYQTGNESLMLSDASDIVLVTTAKAALFIDFD 332
Db 265 MYRAIEEKVHLAQVIKIQNAEKVTVYQT-PAKENMASVTADEVYVCTTSRARRIKE 323	Db 265 MYRAIEEKVHLAQVIKIQNAEKVTVYQT-PAKENMASVTADEVYVCTTSRARRIKE 323
Qy 333 PPLSISKMEALRSVHYDSTSKEELTRFKWEDDGIRGKSSTDGPSRYIYPPSHSPTN 392	Qy 333 PPLSISKMEALRSVHYDSTSKEELTRFKWEDDGIRGKSSTDGPSRYIYPPSHSPTN 392
Db 324 PPLPPKKAHARSVHYRGTKIPLTCMKFWEDBINGKSTTDLPSRFIYPPHNNTSG 383	Db 324 PPLPPKKAHARSVHYRGTKIPLTCMKFWEDBINGKSTTDLPSRFIYPPHNNTSG 383
Qy 393 ETIGVLLASYTWSDESLIFLGLASDEELKELAALRDLAKH--GEQWYDKCTGVIVKWSA 449	Qy 393 ETIGVLLASYTWSDESLIFLGLASDEELKELAALRDLAKH--GEQWYDKCTGVIVKWSA 449
Db 384 -VGVIIA-YGIGDDANFFQALDFKDCADIVINDLQLPREEQTCFIPSMIQKWSL 440	Db 384 -VGVIIA-YGIGDDANFFQALDFKDCADIVINDLQLPREEQTCFIPSMIQKWSL 440
Qy 450 DPYSLGAFALFTPYQHLYEAQELFSSEGRRHFAGEHTAPPHAWIETSMKSARAATNNIK 509	Qy 450 DPYSLGAFALFTPYQHLYEAQELFSSEGRRHFAGEHTAPPHAWIETSMKSARAATNNIK 509
Db 441 DKYAMGGITTFTPYQFOHFSESLTAVDRIFTAGEHTAEAHGWIDSTIKSGLRAARDVNR 500	Db 441 DKYAMGGITTFTPYQFOHFSESLTAVDRIFTAGEHTAEAHGWIDSTIKSGLRAARDVNR 500
Qy 510 VANE 513	Qy 510 VANE 513
Db 501 ASEQ 504	Db 501 ASEQ 504
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ID_OXLA_AGRKH STANDARD; PRT; 516 AA.	
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DT_15-DEC-1998 (Rel. 41, Last sequence update)	
DT_28-FEB-2003 (Rel. 41, Last annotation update)	
DT_25-OCT-2004 (Rel. 45, Last annotation update)	
DR_L-amino-acid oxidase precursor (EC 1.4.3.2) (LAAO) (Apoxin 1).	
DR_Agkistrodon rhodostoma (Malayan pit viper) (Calloselasma rhodostoma).	
OS_Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	
OC_Lepidosauria; Squamata; Scleroglotta; Serpentes; Colubroidea;	
OC_Viperidae; Crotalinae; Calloselasma.	
NCBI_TaxID=8717;	
RN_SEQUENCE FROM N.A., AND SEQUENCE OF 19-33.	
RP_SEQUENCE FROM N.A.; TISSUE=Venom gland;	
RC_MEDLINE=21145410; PubMed=11248687;	
RA_Macheroux P.; Seth O.; Boltschweiler C.; Schwarz M., Kurfuerst M.,	
Au_L.-C.; Ghisia S.; Teng M., Niu L.; RT_Zhang H., Zhang T.,	
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DR_05-JUL-2004 (TREMBLrel. 27, Last annotation update)	
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OS_Agkistrodon halys pallas (Chinese water moccasin) (Gloydius halys pallalis); Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
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NCBI_TaxID=8714;	
RN_MEDLINE=21145410; PubMed=11248687;	
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Au_L.-C.; Ghisia S.; Teng M., Niu L.; RT_Zhang H., Zhang T.,	
RA_R "L-amino-acid oxidase from Malayan pit viper Calloselasma	
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DR_05-JUL-2004 (TREMBLrel. 27, Last annotation update)	
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OC_Viperidae; Crotalinae; Calloselasma.	
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RN_MEDLINE=21145410; PubMed=11248687;	
RA_Macheroux P.; Seth O.; Boltschweiler C.; Schwarz M., Kurfuerst M.,	
Au_L.-C.; Ghisia S.; Teng M., Niu L.; RT_Zhang H., Zhang T.,	
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Au_L.-C.; Ghisia S.; Teng M., Niu L.; RT_Zhang H., Zhang T.,	
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OC_V	

RT rhodostoma:comparative sequence analysis and characterization of active and inactive forms of the enzyme.";  
 RT Pur. J. Biochem. 268:1679-1686(2001).  
 RN [2]

RP SEQUENCE OF 19-38 FROM N.A.  
 RC TISSUE:Venom;

RX MEDLINE=94361525; PubMed=8080286; DOI=10.1006/abbi.1994.1401;

RA Ponnudurai G., Chung M.C.M., Tan N.-H.;  
 RT "Purification and properties of the L-amino acid oxidase from Malayan pit viper (Callobelasma rhodostoma) venom.";  
 RL Arch. Biochem. Biophys. 313:373-378(1994).  
 RN [3]

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS), AND CARBOHYDRATE-LINKAGE SITES.

RC TISSUE:Venom;  
 RX MEDLINE=2042326; PubMed=10944103; DOI=10.1093/embj/19.16.4204;  
 RA Pawelek P.D., Cheah J., Coulombe R., Macheroux P., Ghislain S.,  
 RP Vrielink A.;

RT "The structure of L-amino acid oxidase reveals the substrate trajectory into an enantioselectively conserved active site.";  
 RL J.19:4204-4215(2000);  
 CC -I- FUNCTION: Catalyzes an oxidative deamination of predominantly hydrophobic and aromatic L-amino acids. Has an antibacterial effect and an ability to induce apoptosis. The H(2)O(2) produced by L-amino acid oxidation is involved in the apoxin-I induced apoptosis and hemorrhage caused by the venom.  
 CC -I- CATALYTIC ACTIVITY: An L-amino acid + H(2)O + O(2) = a 2-oxo acid  
 CC + NH(3) + H(2)O(2).  
 CC -I- COFACTOR: FAD.

CC -I- SUBUNIT: Homodimer.

CC -I- MICROSERIAL: Has a pH optimum of 9.0, a determined pI of 4.4 and is temperature stable.

CC -I- SIMILARITY: Belongs to the flavin monoamine oxidase family. Strong to mammalian FGL.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions. There is no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC DR EMBL; PDB; CAB71136; 1; -.

DR PDB; 1B8R; X-ray; A/B/C/D/E/F/G/H=19-516.

DR GlycoSuiteDB; PB1382; -.

DR InterPro; IPR000159; Adrindr reductase.

DR InterPro; IPR001613; Aminoxid fl.

DR InterPro; IPR002337; Amino oxidase.

DR InterPro; IPR00005; NAD(BS).

DR Pfam; PF01593; Amino oxidase; 1.

DR PRINTS; PR00419; ADXRITASE.

DR PRINTS; PR00757; AMINOKYDASE.

KW 3D-structure; Direct protein sequencing; FAD; Flavoprotein;

KW Glycoprotein; Oxidoreductase; Signal; Toxin.

FT SIGNAL 1 18 L-amino-acid oxidase.

FT CHAIN 19 516 FAD (ADP part) (Potential).

FT NP BIND 52 108 N-linked (GlcNAc . . ).

FT CARBOHYD 190 190 N-linked (GlcNAc . . ).

FT CARBOHYD 379 379 C -> E (In Ref. 2).

FT CONFLICT 28 28 D -> N (In Ref. 2).

FT TURN 33 33

FT TURN 24 25

FT HELIX 26 29

FT TUBN 32 33

FT HELIX 34 43

FT STRAND 53 57

FT CONFLICT 60 60

FT HELIX 61 72

FT TURN 73 74

FT STRAND 76 80

FT STRAND 87 87

FT TURN 88 89

FT STRAND 95 99

FT TURN 96 103

FT STRAND 100 110

FT STRAND 109 112

FT TURN 111 122

FT HELIX 114 124

FT TURN 123 130

FT STRAND 127 136

FT TURN 135 141

FT STRAND 138 143

FT TURN 142 147

FT HELIX 148 153

FT TURN 155 158

FT HELIX 164 168

FT TURN 171 178

FT HELIX 179 188

FT TURN 191 197

FT STRAND 198 202

FT HELIX 203 209

FT TURN 210 215

FT HELIX 224 225

FT TURN 225 230

FT HELIX 231 232

FT TURN 234 234

FT HELIX 235 245

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FT STRAND 251 254

FT TURN 255 256

FT STRAND 258 259

FT HELIX 260 268

FT TURN 269 269

FT HELIX 270 272

FT STRAND 273 274

FT TURN 278 284

FT STRAND 289 294

FT STRAND 302 305

FT STRAND 307 310

FT HELIX 314 317

FT TURN 318 319

FT STRAND 321 322

FT HELIX 328 336

FT STRAND 339 340

FT STRAND 342 349

FT HELIX 353 357

FT TURN 358 358

FT STRAND 363 366

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FT STRAND 372 374

FT TURN 381 382

FT STRAND 385 392

FT HELIX 393 393

FT TURN 398 401

FT STRAND 404 418

FT HELIX 419 420

FT TURN 423 429

FT STRAND 430 437

FT HELIX 438 438

FT TURN 442 444

FT STRAND 448 449

FT HELIX 453 454

FT TURN 455 464

FT STRAND 467 467

FT TURN 468 469

FT STRAND 470 472

FT HELIX 475 477

FT MW 503 AA;

FT SEQUENCE 58221 MW;

FT SQ 5F9435718B3A1BDE CRC64;

FT SEQUENCE 39.9%; Score 1079.5; DB 1; Length 516;

Query Match

Best Local Similarity	Best Local Similarity	Pred. No.	2e-57;	Indels	Gaps	Matches	Conservative	Mismatches	Indels	Gaps	Matches
44.4%	44.4%	219	2e-58;	21	5	92	96	96	175	7	5;
Qy	33	LADCLEDKDYDTLLQTLGPHINTSHAVVIVAGMAGLTAAKLUQDAGHTVTILEAND	92	Qy	33	LADCLEDKDYDTLLQTLGPHINTSHAVVIVAGMAGLTAAKLUQDAGHTVTILEAND	92	Qy	33	LADCLEDKDYDTLLQTLGPHINTSHAVVIVAGMAGLTAAKLUQDAGHTVTILEAND	92
Db	25	LAEECQENDYEEFELTARNGKATSNPKVTFIVAGMAGLAAVYVLAGHQTITLEASE	84	Db	25	LAEECQENDYEEFELTARNGKATSNPKVTFIVAGMAGLAAVYVLAGHQTITLEASE	84	Db	25	LAEECQENDYEEFELTARNGKATSNPKVTFIVAGMAGLAAVYVLAGHQTITLEASE	84
Qy	93	RVGGRVTRYNEKEGYAEMGAMRIPSSHRIWVQFWVKLGTVEMNEFVMTDNTFYLVNG	152	Qy	93	RVGGRVTRYNEKEGYAEMGAMRIPSSHRIWVQFWVKLGTVEMNEFVMTDNTFYLVNG	152	Qy	93	RVGGRVTRYNEKEGYAEMGAMRIPSSHRIWVQFWVKLGTVEMNEFVMTDNTFYLVNG	152
Db	85	RPGGRVTRYNEBAGWYANLCPMLRLPEKHRVRETRKFDRNLRENSQENNAWFIKNI	144	Db	85	RVGGRVTRYNEBAGWYANLCPMLRLPEKHRVRETRKFDRNLRENSQENNAWFIKNI	144	Db	85	RVGGRVTRYNEBAGWYANLCPMLRLPEKHRVRETRKFDRNLRENSQENNAWFIKNI	144
Qy	153	RERTYVQENPDVLKYNNSEEGKISADDLDRALOKVKEVEANGCKAALEKRYSVK	212	Qy	153	RERTYVQENPDVLKYNNSEEGKISADDLDRALOKVKEVEANGCKAALEKRYSVK	212	Qy	153	RERTYVQENPDVLKYNNSEEGKISADDLDRALOKVKEVEANGCKAALEKRYSVK	212
Db	145	RKKVGEVKDQFGLLKYPVKPSBAGSAGOLYYEESLGGKVVEBLKRKNCSYINKYDYSTK	204	Db	143	RKRVREVTKNCPCLLEYFKVKPSEEGKSBAQLYYESLRRVVKELKRTNCKYILDKYDTSTK	202	Db	143	RKRVREVTKNCPCLLEYFKVKPSEEGKSBAQLYYESLRRVVKELKRTNCKYILDKYDTSTK	202
Qy	213	EYLBEGGLSFGAVRMIGDLINQEQLMYTALSEMYDQADVNDSTVYTHEVGGSDILPEA	272	Qy	213	EYLBEGGLSFGAVRMIGDLINQEQLMYTALSEMYDQADVNDSTVYTHEVGGSDILPEA	272	Qy	213	EYLBEGGLSFGAVRMIGDLINQEQLMYTALSEMYDQADVNDSTVYTHEVGGSDILPEA	272
Db	205	EYLIKEGDLSFGAVMDYDNLINEDSYYVSTIESLKHDDIPIAYERRFDEIDVGMDKLPTA	264	Db	203	EYLLKGSLNLSGAVIDTIGDLINEDSGYVFSIBSLRHDIFYEKRDEIVGMDQJPLTS	262	Db	203	EYLLKGSLNLSGAVIDTIGDLINEDSGYVFSIBSLRHDIFYEKRDEIVGMDQJPLTS	262
Qy	273	FLSVLVDPVILLNSKYKHIROSKGKVYVSYQTGNQNESSLMDLSADIUVTTAKAALFDID	332	Qy	273	FSLVLDPVILLNSKYKHIROSKGKVYVSYQTGNQNESSLMDLSADIUVTTAKAALFDI	332	Qy	273	FSLVLDPVILLNSKYKHIROSKGKVYVSYQTGNQNESSLMDLSADIUVTTAKAALFDI	332
Db	265	MYRDIODKVNHAQVTKIQCQNDQKVTVVVYETLSKET-PSVTADEVVCTSRVRLIKFN	323	Db	263	MYEAIKEKVQVHFNAVARIEQONDREATVQTOSANEMS-SVYTADEVVCTSRVRLIKFN	320	Db	263	MYEAIKEKVQVHFNAVARIEQONDREATVQTOSANEMS-SVYTADEVVCTSRVRLIKFN	320
Qy	333	FPLSLSKMEARSVYDSDSTKILLFRDKEWDGIGRGKSITDGPSSRYXYPHSISFHTN	392	Qy	330	DFDPPLUSISKNEBALRSVHYDSDSTKILLFRDKEWDGIGRGKSITDGPSSRITYYPHSF	389	Qy	330	DFDPPLUSISKNEBALRSVHYDSDSTKILLFRDKEWDGIGRGKSITDGPSSRITYYPHSF	389
Db	324	PLLPGKAHALRSVYHRSGTKIFLCTTKFWEDDTHGGKSTTDLPSRFIYYPNINF-TN	382	Db	321	KFEPPLPKKAHALRSVYHRSGTKIFLCTTKFWEDDTHGGKSTTDLPSRFIYYPNINF	380	Db	321	KFEPPLPKKAHALRSVYHRSGTKIFLCTTKFWEDDTHGGKSTTDLPSRFIYYPNINF	380
Qy	393	ETIGVLLASVTSWDESLLFGLASDEBELKELAARDLAKIH--GEQWWDKCTGVIVKWSA	449	Qy	390	HTNETIGVLLASVTSWDESLLFGLASDEBELKELAARDLAKIH--GEQWWDKCTGVIVKWSA	446	Qy	390	HTNETIGVLLASVTSWDESLLFGLASDEBELKELAARDLAKIH--GEQWWDKCTGVIVKWSA	446
Db	383	-GIVGTLIA-YGIGDANFFQALDFKDCAIDIVFNDLSLHQLPKDIDQSFPSVIQKWSL	440	Db	381	TSG--VGVLLIA-YGIGDANFFQALDFKDCAIDIVFNDLSLHQLPKDIDQSFPSVIQKWSL	437	Db	381	TSG--VGVLLIA-YGIGDANFFQALDFKDCAIDIVFNDLSLHQLPKDIDQSFPSVIQKWSL	437
Qy	450	DPSLGAFAFLPTPYOHLEYAQBLFSEGRVHAFGHTAHPAWITSMSKAIRATNINK	509	Qy	447	WSADPYSLGAFALPTPYOHLEYAQBLFSEGRVHAFGHTAHPAWITSMSKAIRATNINK	506	Qy	447	WSADPYSLGAFALPTPYOHLEYAQBLFSEGRVHAFGHTAHPAWITSMSKAIRATNINK	506
Db	441	DKYANGGITFTPTQOFQHFSQDPLTASQGRHGWIDSTIKSGLTAARDVNL	500	Db	438	WSDLKYAMGGITTFTPTQOFQHFSQDPLTASQGRHGWIDSTIKSGLTAARDVNL	497	Db	438	WSDLKYAMGGITTFTPTQOFQHFSQDPLTASQGRHGWIDSTIKSGLTAARDVNL	497
Qy	510	VANEESTIETHTKD	522	Qy	507	INKVANEESTIETHTKD	522	Qy	507	INKVANEESTIETHTKD	522
Db	501	ASENPMSGIHLNSD	513	Db	498	VNRASEPNMSGIHLNSD	513	Db	498	VNRASEPNMSGIHLNSD	513

RESULT 6	Q9PWC9	PRELIMINARY;	PRT;	516 AA.
Q9PWC9	Q9PWC9;			
AC	Q9PWC9;			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
FAD-containing L-amino acid oxidase Apoxin 1.				
DE	FAD-containing L-amino acid oxidase Apoxin 1.			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Cetacea; Apoxin 1.			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Cetacea; Apoxin 1.			
QC	Lepidosauvia; Squamata; Scleroglossaa; Serpentes; Colubroidea; Viperidae; Crotalinae; Crotalus.			
OC	Viperidae; Crotalinae; Crotalus.			
OX	NCBI_TaxID=8710;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	SEQUENCE FROM N.A.			
RA	TISSUE=Venom gland; Torii S., Mashima T., Naito M., Haga N., Yamamoto K., FOX J.W., TSURU T.; Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.			
RA	TISSUE=Venom gland; Torii S., Mashima T., Naito M., Haga N., Yamamoto K., FOX J.W., TSURU T.; Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AY98691; AAR1182.1; -.			
DR	GO; GO:0004497; F:monooxygenase activity; IEA.			
DR	InterPro; IPR00759; Adnrdx_reductase.			
DR	InterPro; IPR001613; Aminoxid_f1.			
DR	InterPro; IPR009960; Flavcont_mnoxgn.			
DR	InterPro; IPR000759; Adnrdx_reductase.			
DR	InterPro; IPR002937; Amino oxidase.			
DR	InterPro; IPR000205; NAD_B5.			
DR	InterPro; IPR000103; Pyridine_redox_2.			
DR	Pfam; PF01593; Amtn oxidse_1.			
DR	PRINTS; PR00419; ADXRDXASE.			
DR	PRINTS; PR00469; PNDRDXASEII.			
FT	NON_TER 497			
SQ	SEQUENCE 497 AA:	516 AA;	56288 MW;	51AFCB28038399A1 CRC64;
SQ	SEQUENCE 497 AA:	516 AA;	58766 MW;	6CB90A49A0C015ES CRC64;
Query Match	39.3%	Score 1063.5;	DB 2;	Length 516;
Best Local Similarity	45.1%	Score 1059.5;	DB 2;	Length 497;
Pred. No.	3.3e-57;			

Matches	Conservative	85:	Mismatches	166:	Indels	7:	Gaps	4:
Dy	33	LADCLEDKDYDTLLQTLNDGLPHNNTSHVVIVVAGGMAGLTAAKLQDAGHTVTILEAND	92					
Db	20	LEBECFRRTDYDEBFELAKNGLSRTSNSPKRVYIVVAGMSGSUAAVYLAVAGHQTVYBLEASE	79					
Dy	93	RVGGRVETRYNEKEGHYAEAGSAMRIPSSRRIVQWVFKLGVEMMEFVMTDDNTFLYNGV	152					
Db	80	RAGGQVTKYTRNEKEGHYANLGPMRLDEKRVIREVIRKGLQLINEFSQENENWYFIKNI	139					
Dy	153	RERTYYQQENPDVLKYTNVESEKGISADDILDRALQKVEEVEANGCKAALEKDYRSVK	212					
Db	140	RKRGVEYNKDGVLDPVKVEVGSGAQYEESQKAVEELTRNCSYMLNKYDVYSTK	199					
Dy	213	EYLKEEGGLSPGAVRMIGDLINNEQSUMYTALSEMIDQADVNDSVTYHEVTGGSDLPEA	272					
Db	200	EYLKEGNLSPGAVMIGDLINNEQGYYSFIESLKHDHDFAYEKRFDEIVGGMMDKLPTS	259					
Dy	273	FLSVLVDVPLANSKYKHIIROSDKGTVYSGTGNESLMDLSADIVLVTTTAKAFLIDFD	332					
Db	260	MYQAQEKVHLNARYIKIQDQVKETVTVQT-SEKTELTSVATDVYIVCTARRKFE	318					
Dy	333	PPLSISMEALRSVYIDSSTSILLFRDKEWDDIGRKGSKSITDGPSRYYIYPSSHSPHTN	392					
Db	319	PPLPKKAHAIRSVHYRSGTKIFLCTKFWEDDQIHGKSKSTDLPSPRIYFPNNHFNG	378					
Dy	393	ETIGVLLASYTWSDESILLFLGASDEELKELALRDIAKTH--GEQWWDKCTGTIVKCKMSA	449					
Db	379	--VGVIIA-VGIGDDANYFEALDFDCGDIVINDSLIHLQPKREBIAQACRPSMIQRWSL	435					
Dy	450	DPSISLGAFALFTPYQHLEYAQELFSEGRVHEAGEHTAPHAMITEMSKS	499					
Db	436	DKYAMGCGTTTTPQFOHFSALTYTDPVDRYFAGSYTAQAHGTTASTIS	485					

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RESULT 8		OXLA_CROAD	OXLA_CROAD	STANDARD;	PRT;	516 AA.
O933764;	AC	15-JUL-1999	(Rel. 38, Created)			
O933764;	OT	15-JUL-1999	(Rel. 38, Last sequence update)			
O933764;	OT	25-OCT-2004	(Rel. 45, Last annotation update)			
O933764;	OT		L-amino-acid oxidase precursor (EC 1.4.3.2)	(LAO) (IAAO)	(Apoxin I).	
O933764;	DS		Crotalus adamanteus (Eastern diamondback Rattlesnake).			
O933764;	DC		Crotalus; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			
O933764;	OC		Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;			
O933764;	VC		Viperidae; Crotalinae; Crotalus.			

NCBI\_TaxID=8729;  
[1] -  
SEQUENCE FROM N.A., AND SEQUENCE OF 19-44 AND 106-130.  
TISSUE=venom;  
MEDLINE=93639573; PubMed=9703950; DOI=10.1006/bbrc.1998.9024;  
RAIBAKAS A., MASSEY V.;  
"Primary structure of the snake venom L-amino acid oxidase shows high

homology with the mouse B cell interleukin 4-induced F1g1 protein.<sup>17</sup> Biophys. Res. Commun. 248:476-478 (1998).

-!- FUNCTION: Catalyzes an oxidative deamination of predominantly hydrophobic and aromatic L-amino acids. Has an antibacterial effect and an ability to induce apoptosis. The H(2)O(2) produced by L-amino acid oxidation is involved in the  $\text{Fe}^{2+}$ -induced

**C - I - C** = **C - O - C** + **NH<sub>3</sub>(I)** + **H(2)O<sub>2</sub>** + **CO<sub>2</sub>** + **H<sub>2</sub>O** + **O(2)** = a 2-oxo acid  
**C - I - C** = **C - O - C** + **NH<sub>3</sub>(I)** + **H(2)O<sub>2</sub>** + **CO<sub>2</sub>** + **H<sub>2</sub>O** + **O(2)** = a 2-oxo acid

CO-FACTOR: FAD.  
SUBUNIT: Homodimer.  
PTM: Glycosylated.  
SIMILARITY: Belongs to the flavin monoamine oxidase family.  
STRONG, to mammalian FIG1.  
DATABASE: NAME: Worthington enzyme mammal;  
WWW = <http://www.worthington.biocbem.com/LAO/>.

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OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;	RX MEDLINE=22014058; PubMed=11907037; DOI=10.1074/jbc.M200936200;
OC Viperidae; Crotalinae; trimetresurus.	RA Sun Y.; Nonobe E.; Kobayashi Y.; Kuraishi T.; Aoki F.; Yamamoto K.,
NCBI TaxID=39682;	RA Sakai S.;
RN [1] SEQUENCE FROM N.A.	RT "Characterization and expression of L-amino acid oxidase of mouse milk".
RA Wang J.; Huang Q.; Teng M.; Niu L.; Submitted (JUL-2003) to the EMBL/GemBank/DDJB databases.	RL J. Biol. Chem. 277:19080-19086 (2002).
DR EMBL; AB01382; 1F8R.	DR HSSP; PB1382; 1F8R.
DR HSSP; PB1382; 1F8R.	DR MGD; MGII2140638; LeoI.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.	DR GO; GO:0006115; C:extracellular space; TAS.
DR GO; GO:0061118; P:electron transport; IEA.	DR GO; GO:0001716; F:L-amino-acid oxidase activity; IDA.
DR InterPro; IPR002937; Amino oxidase.	DR GO; GO:0009063; P:amino acid catabolism; IDA.
DR InterPro; IPR0000205; NAD BS.	DR InterPro; IPR000759; Adrinx reducase.
DR InterPro; IPR01593; Amino oxidase; 1.	DR InterPro; IPR001613; Amineoxid fl.
SEQ SEQUENCE 516 AA; 58644 MW; 2E52BD69A13DBA2 CRC64;	DR InterPro; IPR002937; Amino oxidase.
Query Match 38.9%; Score 1052.5; DB 2; Length 516;	DR InterPro; IPR000960; Flav cont_minoxgn.
Best Local Similarity 42.7%; Pred. No. 9.4e-57;	DR InterPro; IPR000205; NAD BS.
Matches 211; Conservative 103; Mismatches 171; Indels 9; Gaps 6;	Pfam; PF01593; Amino oxidase; 1.
Qy 33 LADCDKDYDTLQTLDLGLPHINTSHVTVYAGAGMGLTAAKLJQDAGHTVILEAND	PRINTS; PR00419; ADXRDIASE.
Db 25 LEEEFREDTYEEFELIANGKLATSNPKRVITVAGAGNSGLSAYLAGTGHETVLEASE	PRINTS; PR00757; ANINEOQDASEF.
Qy 93 RVGGRVETYRNKEGWWAEMGMARIPISSHRIQWFWVKLGVMNEFTMDNTFYLVNGV	PRINTS; PR00370; ENOXYGENASE.
Db 85 RAGGRVTRYRNDREBGSWYALPGLPHEGRTRYIKFLNQLNEFSENNDNAWHFVNI	Signal.
Db 85 RAGGRVTRYRNDREBGSWYALPGLPHEGRTRYIKFLNQLNEFSENNDNAWHFVNI 144	FT SIGNAL 1 26 Potential.
Qy 153 RERTYVQENPDVLYKVNSESEKGISADDLBALQKVKEEVANGKALEYDRYSVK	FT CHAIN 27 523 AA; 58587 MW; 8C5A4 FE833BA1ABC1 CRC64;
Db 145 RKTVGEVKRDKPGYLKYKPKPSEEGKSNEQLYBESELREVEKEKLKRTNCSYILNKYDTSTK	FT SEQUENCE 523 AA; 58587 MW; 8C5A4 FE833BA1ABC1 CRC64;
Qy 213 EYIKEEGLSPGAVRMIGDLNNEQSILNLYTALESE-MYIQDQADVNDSVTTYHEYGGSDLLPE	Query Match 38.8%; Score 1049.5; DB 2; Length 523;
Db 205 EYIKEEGLSPGAVRMIGDLNNEQSILNLYTALESE-MYIQDQADVNDSVTTYHEYGGSDLLPE 271	Best Local Similarity 43.5%; Pred. No. 1.7e-56;
Qy 272 AFLSVLDPILLNSKVKHROSDKGIVTYSQTGNESISSLMLSDASDIVLVTTTAKAALFD	Matches 226; Conservative 79; Mismatches 166; Indels 49; Gaps 7;
Db 264 SMYRAIEEKVHNAQVIRIKQNAEVTYVQT-PEKDTSFTADYVCTVCTSGAARRIKF	Qy 27 LSLKELHADLCEDKDYDTLQLTDNLGPHINTSHVTVYAGAGMGLTAAKLJQDAGHTV 86
Db 332 DPPLSISMEALRSVHYDSSTSKEFLKDFKWEFDDGTRGCKSITDOPSRVITYPSHSFHT	Db 25 LALYBNLVKCFQDPYEAFPLIAQNLGHTSPLSKVPPVYVAGAGMGLTAAKLJQDAGHTV 84
Qy 323 EPLLPLKAHLRSVHYRGTKFLTCFKFLCTKFWDEGIGHGGSTTDLPSRFIYYPHNFTS	Qy 87 ILEANDRVRGGRVETYRNKEGWWAEMGMARIPISSHRIQWFWVKLGVMNEFTMDNTFDDNTF 146
Db 392 NETIGVLLASYTWSDESILFLGASDEEKKELALRDIAKIH--GEQWVDRCTGVTKWNS	Db 85 ILEASHNHIGRVRVTLRKNEKEWLGPMPRIPESKHLIITYVQQLGKUNKFNQYDSNTW 144
Db 383 G--VGVLIA-YGTGDDANFQALDQKDFIVINDSLHOLPREIQTCPMSMQKWS	Qy 147 YLVNGVRETRYVQENPDVLYKVNSESEKGISADDLBALQKVKEEVANGKALEY 206
Qy 449 ADPYSLGFALFPTPYQHLEYAQELVHAGFAGTAAFHAWLETSMKSAIRATNLIN	Db 145 YLNGQRYASEVANPGLGYPRPSEKNKTVTDLFYQAITKIPHRKTNSNCQLLSSLY 204
Db 440 LDKYAMGGITTFTPYQFOHFSEALTHSDVRYFAGETAHARGWDSSLSKGLTAARDV	Qy 207 DRYSTKEYLKEEGGSLSPGAVRMIGDLNNEQSILNLYTALESEMYDADVNDSVT--YHEVTG 264
Qy 509 KVANEESTIETHKD 522	Db 205 DSYSTKAYLMKEGTJSKRAH-----DRGYNDENAGYKSKRAH----- 243
Db 500 RAISENPSCHLNSD 513	Qy 265 GSD---LIPEAFL-----SVLDPILLNSKVKHROSDKGIVTYSQTGNESISSLMLSDASDIVLVTTTAKAALFD
RESULT 12	Db 244 VSEDCCKHLLQKCP1IRDHRWLCP1PNGLSASLKPQTIRLWSKVERVVRDGPVKVMMYRTD 303
Q9JKK6 PRELIMINARY; PRT; 523 AA.	Db 304 GPTSLILHKJLADYAITASAKAPLITFOPPLSREKTHALRSVHTSATKVKVLYCNERFW 363
ID Q9JKK6 PRELIMINARY; PRT; 523 AA.	Qy 364 EDDGIRGGKSITDGPSPRYIYPSPHSFHTNETIGVIALASYTWSDESLLFIGASDEELKELA 423
AC Q9JKK6 PRELIMINARY; PRT; 523 AA.	Db 364 EODGIRGGSYITDGPSPRYIYPSPHSFHTNETIGVIALASYTWSDESLLFIGASDEELKELA 423
DT 01-OCT-2000 (TREMBLrel. 15, Created)	Qy 424 LRDLAKIH--GEQWVDIKCTGVIVKWKSAADPYSLGAFLPFTPYQHLEYAQELFSSBGRVH 480
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)	Db 422 LDDLAIAVTRIPEKEELKRMCPKSAIKHWSLDPLTGAEFTFPQFQVDYSKQLSQPEGRVY 481
DE L-amino acid oxidase precursor.	Qy 481 FAGHATAFPHAWIETMSKSAIRATNINKVANESTIETH 520
GN Name=Lao1; Synonyms=mIAO;	Db 482 FAGEHTCLPHSWIDAIKGIRASNCIQAAVDEKAETRUGHT 521
OS Mus musculus (Mouse);	RESULT 13
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	FIG1_MOUSE STANDARD;
OX NCBI_TAXID=10090;	AC 009046; Q9CKK7;
RN [1] SEQUENCE FROM N.A.	AC 15-DEC-1998 (Rel. 37, Created)
RC STRAIN=ICR; TISSUE=Mammary gland;	DT 15-DEC-1998 (Rel. 37, Last sequence update)

05-JUL-2004 (Rel. 44, Last annotation update)  
 DT DE Interleukin-4 induced protein 1 precursor (Fig-1 protein) (mFIG1).  
 GN Name=1441; Synonyms=ig1;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1] RPPRSEQUENCE FROM N.A.  
 RC STRAIN=BALB/C, and CBA/J;  
 RX MEDLINE=97225983; PubMed=9122225; DOI=10.1073/pnas.94.6.2507;  
 RA Chu C.C., Paul W.E.;  
 RT "Fig1, an interleukin-4-induced mouse B cell gene isolated by cDNA  
 representational difference analysis.",  
 Proc. Natl. Acad. Sci. U.S.A. 94:2507-2512 (1997).  
 RL [2] RPPSEQUENCE OF 122-289 FROM N.A.  
 RC STRAIN=BALB/C; TISSUE=Spleen;  
 RX MEDLINE=99012997; PubMed=9798653; DOI=10.1016/S0161-5890(98)00031-5;  
 RA Chu C.C., Paul W.E.;  
 RT "Expressed genes in interleukin-4 treated B cells identified by cDNA  
 representational difference analysis.",  
 Mol. Immunol. 35:487-502 (1998).  
 RL [3] RPPSEQUENCE OF 217-630 FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Embryonic head;  
 RX MEDLINE=22-5468; PubMed=1246681; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaido I., Osarco N., Saito R., Suzuki H., Yananaka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schrimpf L.M., Kanapin A., Matsuda H., Batzelov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.B., Cousins S.,  
 RA Dalla E., Draganji T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Garibaldi M., Giassi C., Godzik A., Gough J.,  
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konagaya A., Kurochkin I.V., Lee P.A., Lyons P.A.,  
 RA Magliocci D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavav W.J., Peretea G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
 RA Sultan A., Takenaka Y., Taylor M.S., Teasdale B.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Yuan L.G., Wynn-Shore Boris A., Yangaisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arikawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imorani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.,  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.",  
 RL Nature 420:563-573 (2002).  
 CC -I- COFACTOR: FAD (Potential).  
 CC -I- INDUCTION: By interleukin-4.  
 CC -I- SIMILARITY: Belongs to the flavin monoamine oxidase family.  
 CC Strong, to snake L-amino acid oxidase.

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DR EMBL; AK014297; BAB29253.1; ALT\_INIT.  
 DR HSSP; P81382; 1F8R.  
 DR MGI; MGI:109552; II411.  
 DR InterPro; IPR000759; Adrinx\_reductase.  
 DR InterPro; IPR001613; AminoOxid\_F1.  
 DR InterPro; IPR002937; Amino oxidase.  
 DR InterPro; IPR000205; NAD\_B5.  
 DR Pfam; PF01593; Amino\_Oxidase; 1.  
 DR PRINTS; PR00419; ADKDTASE.  
 DR PRINTS; PR00757; AMINEOXDASEF.  
 KW PAD; Flavoprotein; Oxidoreductase; Signal.  
 FT SIGNAL 1 21  
 FT CHAIN 22 61  
 FT NP\_BIND 59 115  
 FT CARBOHYD 53 53  
 FT CARBOHYD 133 133  
 FT CARBOHYD 219 219  
 FT CONFLICT 385 385  
 FT CONFLICT 598 630  
 SQ SEQUENCE 630 AA: 70190 MW: 47500 GPDQTDHLH (in Ref. 3);  
 SQ SEQUENCE 630 AA: A674C5D6D089A071 CRC64;  
 Query Match 38.3%; Score 1034; DB 1;  
 Best Local Similarity 43.5%; Pred. No. 1.7e-55;  
 Matches 212; Conservative 100; Mismatches 163; Indels 12; Gaps 6;  
 Qy 26 ALSLKEHLADCLIEDKCYDYLQTLNDLPLHNTSHSHVIVGAGMAGLTAAKLUQDAGHTY 85  
 Db 25 AASSSLPIEKCMDHDYEQLLKVVTLGLNRTSPQPKVvvVAGVAGVIAKMLSDAGHKV 84  
 Qy 86 TLEADNRVGRVETVRNEKGWYAENGAMRIPSHRIIVQWFVKLGQVEMNBPFVMTDDT 145  
 Db 85 TILEADNRIGRGRIFTDEKGWIGEIGAMMMPSSHRLKLCRUTGLNLTOFTQDENT 144  
 RA 146 FYLVNGVRERTTYVQENPDVLRKNSSESEKGISADDLQLRQKVEBEANGCAALEK 205  
 RA 147 :|: ;|: |:|: ;|: |:|: ;|: |:|: ;|: |:|: ;|: |:|: ;|: |:|: ;|: |:|:  
 RA 148 WTEVHVNTRKLNRVTVKMPKELQYGLYNANRERGHSPEDTYQMALINKAFDLKALGCKKAMNK 204  
 Qy 206 YDRYSYKEYLKEEGGLSPGAVRMIGDILNEQSLMTALSEMYQDADVNDSVTYHEVTGG 265  
 Db 205 FNKHTLLEYLLEGINSRSPVQGLDMSGFFPSAEEAHCLSDRILRSYRIVGG 264  
 RA 266 SDLPLPAAFLSYLDVPLILLNSKVKHRSQDKKVIVSTQTGNESSLMDLSADTVLTTAKA 325  
 RA 267 WDLPPLRALSSSUSGALLNAPEVVSQGRNDVYRHATSLHSE-KTILTADVVVLASGPV 323  
 RA 326 ALFIDDPPLATSKMEALRSVHYDSSTKILLFRDKFWEDDGIRGKRSITDGPSPRTIYP 385  
 RA 324 LQRITSPPLTRKQBALRALHYVAAASKVFLSFRPFWHEHIEGHSNTDRPSRLIFYP 383  
 Qy 386 SHSFHTNETGVLLASVYTWSDESLFLPGASDPELKLALAKTHGE---QWMDKCTGV 442  
 Db 384 ARGEGLS---LLLAStYTWSDAAAPAGPLSDQTILRLVQDVAALGPVVERLWDG-RGV 437  
 Qy 443 IVKKRNADPSYLSGFALFTPYQHLEYAQELRSSE GRVHFAGEHTAFPHAMIEETMSKSAI 501  
 Db 438 -VKRRAEDPHSGGGFVYQPPPLYGRRAEDYDWASAPPGRFVYAGEHTALPHGMVETAVKSGL 496  
 CC RESULT 14  
 CC Q6YBV6 PRELIMINARY; PRT; 630 AA.  
 CC ID Q6YBV6; PRELIMINARY; PRT; 630 AA.  
 CC AC Q6YBV6; PRELIMINARY; PRT; 630 AA.  
 CC DT 05-JUL-2004 (TREMBLref. 27, Created)  
 CC DT 05-JUL-2004 (TREMBLref. 27, Last sequence update)  
 CC DT 05-JUL-2004 (TREMBLref. 27, Last annotation update)  
 CC DE Interleukin-four induced gene-1 protein.  
 GN Name=II411;

OS Mus musculus (Mouse). Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. OC NCBI\_TaxID=10090; RN [1] SEQUENCE FROM N.A. STRAIN=NZN. SEQUENCE FROM N.A.

RC STRAIN=NZN. SEQUENCE FROM N.A.

RA C.C., Kim J.A., Hsueh K.; Chu C.C., Kim J.A., Hsueh K.; RA Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases. RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases. DR EMBL; AY157538; AAO17039\_1; -. DR EMBL; AY157537; AAO17038\_1; -. DR GO; GO:0016491; F:oxidoreductase activity; IEA. DR GO; GO:0006118; P:electron transport; IEA. DR InterPro; IPR00059; Adrkd\_reductase. DR InterPro; IPR001613; Amino oxid\_f1. DR InterPro; IPR002937; Amino oxidase. DR InterPro; IPR000205; NAD\_B5. DR Pfam; PF01593; Amino oxidase; 1. DR PRINTS; PR00419; ADXRDTASE. DR PRINTS; PR0057; AMINEODASEF. DR SEQUENCE 630 AA; 70294 MW; SA90C0B1B29D9095 CRC64;

Query Match 38.3%; Score 1034; DB 2; Length 630; Best Local Similarity 43.5%; Pred. No. 1.7e-55; Matches 212; Conservative 100; Mismatches 163; Indels 12; Gaps 6;

Qy 26 ALSLKEHADCLEDKDVTLLQLDNGPHINTSHVTLQGLNLTQAKLQLDAGHTV 85 Db 25 RASSLNPIEKCMDHDVQLLKVTGLNRPISKPQRTVVGAGVAVLAAKMLSDAGHKV 84 Qy 86 TLEANDRVRGGRVETYNEKEGWAENGAMRIPPSSHRIVONFVKKGUVEMNEFVMTDDNT 145 Db 85 TLEADRNIGGRIFFTRDEKIGTWIGELGAMRMPSSHRLAKLCRTGLNUTQFTOYDENT 144 Qy 146 FYLVNGVREPTYQENPDVLYKVNSEEGKISADDLILRALKREEVANGKALEX 205 Db 145 WTEVHNVLRLNRTVVEKQPKLGYNLRNRRGHSPEDYQMLNKAFLKALGCKAMNK 204 Qy 206 YDRYSVKEYLKREGGLSPGAVRMIGDLNEQSMLTALSEMIYDADVNDSVTYHEVTGG 265 Db 205 FNKHTLLEVLEGNLSRPAVQJGDVMSEEFGYLSPEALRAHACSDRLRYSRIVGG 264 Qy 266 SDLLBEAFLSVDLVEILLNSKVRHITRODSKGTVIYSGOTNESSLMDSLADIVLVTTAKA 325 Db 265 WDLLRALLSSLSGALLNAPVUSTQGRNDVRVHATSLHSE-KTLDADVLLTAGSPA 323 Qy 326 ALFTDFPPLSISKMEALSRSVHYDSTKLLTFRDKFWDDGTRGKSTSITDGPSRYIYP 385 Db 324 LQRITFSPLTRKRREALHVAASKVFLSPRPFWHEHIGHSNTDRPSRLIFYP 383 Qy 386 SHSFHTNETIGVLLASYTWSDESLFLGASDEELKLRLDAKTHGE -- QWDKCTGV 442 Db 384 ARGES: ---LILASYTWSDAAAPFAGASTDQTLLRLQDVAAHGPVYFRWLWG-RGV 437 Db 384 AGCEGS: ---LILASYTWSDAAAPFAGASTDQTLLRLQDVAAHGPVYFRWLWG-RGV 437 Db 324 LORITFSPLTRKRREALHVAASKVFLSPRPFWHEHIGHSNTDRPSRLIFYP 383 Qy 386 SHSFHTNETIGVLLASYTWSDESLFLGASDEELKLRLDAKTHGE -- QWDKCTGV 442 Db 384 ARGES: ---LILASYTWSDAAAPFAGASTDQTLLRLQDVAAHGPVYFRWLWG-RGV 437 Db 443 IVKKWSADPYSIGAFALFTPYOHLEYAQELPSS-EGRVHFAGENTAFPHWIETSMSKAI 501 Db 438 -VKRWAEDPHSGQGFVYQPPLYGREAAEDYDWSAPPRIYFAGENTALPHGWETAVKSGL 496 Qy 502 RAATNIN 508 Db 497 RAAVRIN 503

Search completed: October 4, 2005, 14:00:54  
Job time : 193 secs

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. OC NCBI\_TaxID=10090; RN [1] SEQUENCE FROM N.A. RC STRAIN=NZN. SEQUENCE FROM N.A.

RA C.C., Kim J.A., Hsueh K.; Chu C.C., Kim J.A., Hsueh K.; RA Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases. RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases. DR EMBL; AY157538; AAO17039\_1; -. DR EMBL; AY157537; AAO17038\_1; -. DR GO; GO:0016491; F:oxidoreductase activity; IEA. DR GO; GO:0006118; P:electron transport; IEA. DR InterPro; IPR000759; Adrkd\_reductase. DR InterPro; IPR001613; Amino oxid\_f1. DR InterPro; IPR002937; Amino oxidase. DR InterPro; IPR000205; NAD\_B5. DR Pfam; PF01593; Amino oxidase; 1. DR PRINTS; PR00419; ADXRDTASE. DR PRINTS; PR0057; AMINEODASEF. DR SEQUENCE 630 AA; 70294 MW; SA90C0B1B29D9095 CRC64;

Query Match 38.3%; Score 1034; DB 2; Length 630; Best Local Similarity 43.5%; Pred. No. 1.7e-55; Matches 212; Conservative 100; Mismatches 163; Indels 12; Gaps 6;

Qy 26 ALSLKEHADCLEDKDVTLLQLDNGPHINTSHVTLQGLNLTQAKLQLDAGHTV 85 Db 25 RASSNPICMEDDYEQILKVTQILNARTSKPQKVYVAGAGMGLTAARKLQLDAGHTV 84 Qy 86 TLEANDRVRGGRVETYNEKEGWAENGAMRIPPSSHRIVONFVKKGUVEMNEFVMTDDNT 145 Db 85 TLEADRNIGGRIFFTRDEKIGTWIGELGAMRMPSSHRLAKLCRTGLNUTQFTOYDENT 144 Qy 146 FYLVNGVREPTYQENPDVLYKVNSEEGKISADDLILRALKREEVANGKALEX 205 Db 145 WTEVHNVLRLNRTVVEKQPKLGYNLRNRRGHSPEDYQMLNKAFLKALGCKAMNK 204 Qy 206 YDRYSVKEYLKREGGLSPGAVRMIGDLNEQSMLTALSEMIYDADVNDSVTYHEVTGG 265 Db 205 FNKHTLLEVLEGNLSRPAVQJGDVMSEEFGYLSPEALRAHACSDRLRYSRIVGG 264 Qy 266 SDLLBEAFLSVDLVEILLNSKVRHITRODSKGTVIYSGOTNESSLMDSLADIVLVTTAKA 325 Db 265 WDLLRALLSSLSGALLNAPVUSTQGRNDVRVHATSLHSE-KTLDADVLLTAGSPA 323 Qy 326 ALFTDFPPLSISKMEALSRSVHYDSTKLLTFRDKFWDDGTRGKSTSITDGPSRYIYP 385 Db 324 LQRITFSPLTRKRREALHVAASKVFLSPRPFWHEHIGHSNTDRPSRLIFYP 383 Qy 386 SHSFHTNETIGVLLASYTWSDESLFLGASDEELKLRLDAKTHGE -- QWDKCTGV 442 Db 384 ARGES: ---LILASYTWSDAAAPFAGASTDQTLLRLQDVAAHGPVYFRWLWG-RGV 437 Db 443 IVKKWSADPYSIGAFALFTPYOHLEYAQELPSS-EGRVHFAGENTAFPHWIETSMSKAI 501 Db 438 -VKRWAEDPHSGQGFVYQPPLYGREAAEDYDWSAPPRIYFAGENTALPHGWETAVKSGL 496 Qy 502 RAATNIN 508 Db 497 RAAVRIN 503

RESULT 15  
Q6YD18 PRELIMINARY: PRT; 630 AA.  
AC Q6YD18; DT 05-JUL-2004 (T-EMBLrel. 27, Created)  
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)  
DB InterPro-4 induced gene-1 protein.  
GN Name=1141i.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Copyright GenCore version 5.1.6  
(c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2005, 13:43:40 : Search time 79 Seconds  
(without alignments)  
1162.663 Million cell updates/sec

Title: US-10-645-094-1

Perfect score: 2703 MNLHVKWKLSVNVLITY.....TNINKVANEESTIETHTKDEL 524

Sequence: 1

Scoring table: BL0S062 Gapop 10.0 , Gapext 0.5

Searched: 800245 seqs, 175286937 residues

Total number of hits satisfying chosen parameters: 800245

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing First 45 summaries

Database : Pending\_Patents\_AA\_New:  
1: /cgn2\_6/ptodata/2/paa/PTC NEW COMB.pep:  
2: /cgn2\_6/ptodata/2/paa/US06 NEW COMB.pep:  
3: /cgn2\_6/ptodata/2/paa/US07 NEW COMB.pep:  
4: /cgn2\_6/ptodata/2/paa/US08 NEW COMB.pep:  
5: /cgn2\_6/ptodata/2/paa/US09 NEW COMB.pep:  
6: /cgn2\_6/ptodata/2/paa/US10 NEW COMB.pep:  
7: /cgn2\_6/ptodata/2/paa/US11 NEW COMB.pep:  
8: /cgn2\_6/ptodata/2/paa/US60 NEW COMB.pep:  
\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query Score	Match	Length	DB ID	Description
1	999	37.0	567	1 PCT-US03-28361-44	Sequence 44, App1
2	999	37.0	567	6 US-10-90-328A-11737	Sequence 11737, A
3	999	37.0	567	6 US-10-152-381B-476	Sequence 476, App1
4	999	37.0	567	7 US-11-055-607-84	Sequence 84, App1
5	407	15.1	478	6 US-10-166-087B-48	Sequence 48, App1
6	294	10.9	545	6 US-10-940-774A-11442	Sequence 11442, A
7	288	10.7	520	1 PCT-US03-09248-13	Sequence 13, App1
8	288	10.7	520	1 PCT-US03-10870-447	Sequence 447, App1
9	288	10.7	520	1 PCT-US03-10870-448	Sequence 448, App1
10	288	10.7	520	6 US-10-390-328A-8287	Sequence 8287, Ap
11	288	10.7	520	6 US-10-390-328A-8288	Sequence 8288, Ap
12	288	10.7	520	7 US-11-051-454-252	Sequence 252, App1
13	283	10.5	527	1 PCT-US03-09248-11	Sequence 11, App1
14	283	10.5	527	1 PCT-US03-10870-549	Sequence 549, App1
15	283	10.5	527	6 US-10-990-328A-8290	Sequence 8290, Ap
16	283	10.5	527	6 US-10-990-328A-8291	Sequence 8291, Ap
17	283	10.5	527	6 US-10-990-328A-8292	Sequence 8292, Ap
18	283	10.5	527	7 US-11-051-454-250	Sequence 250, App1
19	283	10.5	531	6 US-10-940-774A-11443	Sequence 11443, A
20	271	10.0	520	1 PCT-US03-11532-3348	Sequence 1348, App1
21	271	10.0	890	7 US-11-097-143-25362	Sequence 25362, A
22	271	10.0	890	7 US-11-097-143-32703	Sequence 32703, A
23	263.5	9.7	730	1 PCT-US05-13850-1179	Sequence 1179, Ap
24	252.5	9.3	619	7 US-11-072-512-2472	Sequence 2472, App1
25	238	8.8	906	6 US-10-450-763-51651	Sequence 51651, A

## ALIGNMENTS

RESULT 1  
PCT-US03-28361-44

Sequence 44, Application PC/TUS0328361

GENERAL INFORMATION:

APPLICANT: GENENTECH, INC.  
ADDRESS: 1000 Corporate Park Drive, South San Francisco, CA 94080-2100  
CITY: South San Francisco  
STATE: CA  
ZIP: 94080-2100

APPLICANT: SARAH C. BODARY  
ADDRESS: 1000 Corporate Park Drive, South San Francisco, CA 94080-2100  
CITY: South San Francisco  
STATE: CA  
ZIP: 94080-2100

APPLICANT: HILARY CLARK  
ADDRESS: 1000 Corporate Park Drive, South San Francisco, CA 94080-2100  
CITY: South San Francisco  
STATE: CA  
ZIP: 94080-2100

APPLICANT: BRISDELL HUNTE  
ADDRESS: 1000 Corporate Park Drive, South San Francisco, CA 94080-2100  
CITY: South San Francisco  
STATE: CA  
ZIP: 94080-2100

APPLICANT: JANET K. JACKMAN  
ADDRESS: 1000 Corporate Park Drive, South San Francisco, CA 94080-2100  
CITY: South San Francisco  
STATE: CA  
ZIP: 94080-2100

APPLICANT: JILL SCHOENFELD  
ADDRESS: 1000 Corporate Park Drive, South San Francisco, CA 94080-2100  
CITY: South San Francisco  
STATE: CA  
ZIP: 94080-2100

APPLICANT: P. MICKEY WILLIAMS  
ADDRESS: 1000 Corporate Park Drive, South San Francisco, CA 94080-2100  
CITY: South San Francisco  
STATE: CA  
ZIP: 94080-2100

APPLICANT: THOMAS D. WU  
ADDRESS: 1000 Corporate Park Drive, South San Francisco, CA 94080-2100  
CITY: South San Francisco  
STATE: CA  
ZIP: 94080-2100

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF IMMUNE SYSTEM DISORDERS

FILE REFERENCE: P19751 PCT

CURRENT APPLICATION NUMBER: PCT/US03/28361

CURRENT FILING DATE: 2003-09-10

PRIOR APPLICATION NUMBER: US 60/410,174

PRIOR FILING DATE: 2002-09-11

NUMBER OF SEQ ID NOS: 104

SEQ ID NO: 44

LENGTH: 567

TYPE: PRT

ORGANISM: Homo sapiens

PCT-US03-28361-44

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 3 LHVVKWLSSVSVLTTYYSHT-VALSLKSHLADCLEDKDYLQDTLQLDNLSPHNTSHH 61

Db 6 LHLD---LVLPILLSVAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 62 VVIVAGMAGHTAAKULLQDAGHTVTLLEANDRVCGRVETYRNKEKGWYAEMGAMRIPSSH 121

Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

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Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

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Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

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Query 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

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Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

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Query 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

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Query Match 37.0%; Score 999; DB 1; Length 567;

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Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

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Query Match 37.0%; Score 999; DB 1; Length 567;

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Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

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Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

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Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Db 62 VVIVAGVAGVAVAAVQDWKERSQDPFEKMQDPYDQEQLKVVTGLNRPLKPCR 61

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 1.4e-65;

Matches 217; Conservative 99; Mismatches 171; Gaps 9;

Query 62 VVIVAGV

417 RIALDDVAALHGPVVRQLWDG-TGV-VKRWADQHSGGGFVVQPP-----ALWOTEK 466

Db 242 SFAEALRAAISCLSDRQLQYSPRIVGGDWLFLRALLSSILGIVLNAPVYAMTQGPBDHVHQI 301

Qy 302 QTGNES-SLMDSADIVLTTAKAALFIDFPPLSISMEALRSVHYDSTSCKILLFRD 360

Db 302 ETPSPARNLKVLKADVVLTLTASGPAVKRITTSPLPRLMREAFRRHYPATKVYLSPR 361

Db 361 KFWEDDGIIGGKSITDGPSPRYIYPPSHSFHTNETIGVLLASYTWSDESLFLGASDEELK 420

Qy 362 PFWREBHEHGSNTDRPBMIFYP----PREGALLASYTWSDAAAFAULSREPAL 416

Db 421 EIALRDLAKHG---EQWDKCTGIVLUKTMASADPSLGFALFTPYQHLEYAQELFSE 476

Qy 417 RLALDDVAALHGPVVRQLWDG-TGV-VKRWADQHSGGGFVVQPP-----ALWOTEK 466

Db 477 -----GRYHFAEGHTAHPHAWIETSMGSAIRATNN 508

Qy 467 DDTWTPYGRYIYPPGEHTAHPHAWIETSMGSAIRATNN 505

Db 467 DDTWTPYGRYIYPPGEHTAHPHAWIETSMGSAIRATNN 505

RESULT 3  
US-10-152-381B-476  
; Sequence 476, Application US/10152381B  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritson, Mary E.  
; APPLICANT: Godowski, Paul  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanahe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACID  
; TITLE OF INVENTION: SAME  
; FILE REFERENCE: 39870-3330R1C09  
; CURRENT APPLICATION NUMBER: US/10/152-381B  
; CURRENT FILING DATE: 2000-05-21  
; PRIOR APPLICATION NUMBER: US 10-028, 072  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: PCT/US00/32678  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: US 60/187, 202  
; PRIOR FILING DATE: 2000-03-03  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO: 11737  
; LENGTH: 567  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-990-328A-11737

RESULT 2  
US-10-990-328A-11737  
; Sequence 11737, Application US/10990328A  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele  
; TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO1495  
; CURRENT APPLICATION NUMBER: US/10/990-328A  
; CURRENT FILING DATE: 2004-11-17  
; NUMBER OF SEQ ID NOS: 55884  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 11737  
; LENGTH: 567  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-990-328A-11737

Query Match 37.0%; Score 99; DB 6; Length 567;  
Best Local Similarity 41.8%; Pred. No. 1.4e-65;  
Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

Qy 3 LHVVVKWLSSVSVLITYSHT-VALSLKEHLADCLEDKOYDTLQLTGLNGLPHINTSHH 61

Db 6 LHL---LVLPILLSLVVAQDWAERSODPFPEKCMQDPYEQLLKVTWGLNRLTKPQR 61

Qy 62 VVIVGAGAGTAKKLQDAGHTVILEANDRVRGGVETNEKRGWYAEMGARLIPSSH 121

Db 62 VIVQWFGVAGLVAAYKLSDAGHKVTLIADNRIGRIFTRDQNTGWIGLGAHRMPSSH 121

Qy 122 RIVQWFYKLGIVEMNEFVMTDNTFYLNGVTRTYVQVHYNVSESEKGISADD 181

Db 122 RTLHKLCQGLGILNLTKEPOYDNTVVEHEYKLRNVVEKPEKLYALRPQEKGHSPE 181

Qy 182 LLDRALQKVKVEEANGKAALEKYDRYSVKEYLKEEGGLSPGAVRMGIDLNEQSLMYT 241

Db 182 IYQMLNQALKDQLKCKRKAMKKFERHTLILYLLGEGNLNSRPAVOLGDGMSEDFFYL 241

Qy 242 ALSEMIVYQADVNDSVTYHEVTGGSDLLPEAFLSVLDVPIILNSKVYKHROSDFKGYVSY 301

Db 242 SFAEALRAAISCLSDRQLQYSPRIVGGDWLFLRALLSSILGIVLNAPVMTQGPBDHVHQI 301

Qy 302 QTGNES-SLMDSADIVLTTAKAALFIDFPPLSISMEALRSVHYDSTSCKILLFRD 360

Db 302 ETPSPARNLKVLKADVVLTLTASGPAVKRITTSPLPRLMREAFRRHYPATKVYLSPR 361

Qy 361 KFWEDDGIIGGKSITDGPSPRYIYPPSHSFHTNETIGVLLASYTWSDESLFLGASDEELK 420

Db 362 PFWREBHEHGSNTDRPBMIFYP----PREGALLASYTWSDAAAFAULSREPAL 416

Db 421 EIALRDLAKHG---EQWDKCTGIVLUKTMASADPSLGFALFTPYQHLEYAQELFSE 476

Qy 421 EIALRDLAKHG---EQWDKCTGIVLUKTMASADPSLGFALFTPYQHLEYAQELFSE 476

Db 467 DDTWTPYGRYIYPPGEHTAHPHAWIETSMGSAIRATNN 505

Db 477 -----GRYHFAEGHTAHPHAWIETSMGSAIRATNN 508

Db 477 DDTWTPYGRYIYPPGEHTAHPHAWIETSMGSAIRATNN 505

**RESULT 4**

US-11-025-667-84  
 Sequence 64, Application US/110256607  
 GENERAL INFORMATION:  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Boststein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gao, Wei-Oiang  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, Christopher J.  
 APPLICANT: Hillan, Kenneth J.  
 APPLICANT: Pan, James  
 APPLICANT: Poni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Smith, Victoria  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same

FILE REFERENCE: P2330P1C1

CURRENT APPLICATION NUMBER: US/11/025,607  
 CURRENT FILING DATE: 2004-12-28  
 PRIOR APPLICATION NUMBER: US/09/946,374  
 PRIOR FILING DATE: 2001-09-04  
 PRIOR APPLICATION NUMBER: 60/098716  
 PRIOR FILING DATE: 1998-09-01  
 PRIOR APPLICATION NUMBER: 60/098723  
 PRIOR FILING DATE: 1998-09-01  
 PRIOR APPLICATION NUMBER: 60/098749  
 PRIOR FILING DATE: 1998-09-01  
 PRIOR APPLICATION NUMBER: 60/098750  
 PRIOR FILING DATE: 1998-09-01  
 PRIOR APPLICATION NUMBER: 60/098803  
 PRIOR FILING DATE: 1998-09-02  
 PRIOR APPLICATION NUMBER: 60/098821  
 PRIOR FILING DATE: 1998-09-02  
 PRIOR APPLICATION NUMBER: 60/099536  
 PRIOR FILING DATE: 1998-09-09  
 PRIOR APPLICATION NUMBER: 60/099596  
 PRIOR FILING DATE: 1998-09-09  
 NUMBER OF SEQ ID NOS: 477  
 LENGTH: 567  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 us-11-025-667-84

Best Local Similarity 41.8%; Pred. No. 1.4e-65; Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

Qy 361 KFWEDDGTRGGKSTTDGPGSRYIYYPHSHSPHTNTBGTWLSAYTWSDESSLFLUGASDEBLK 420  
 Db 362 PFWREEEHTEGGHSNTDRSSRMITYFP----PPREGA/LIAYSTWSDAAAFAGLSREAL 416  
 Qy 421 ELALRDLAKIHG--EQWDKCTGIVVICKWSSADPYSLGAFALFTPYOHELEYAQELFSE- 476  
 Db 417 RIALDDVAALHGPPVRQLWDG-TGV-VKWWAEDQHSQGFVWQPP-----ALNOTEK 466  
 Qy 477 -----SRVHFAGENTPHAVETETSMKSAIRATNN 508  
 Db 467 DDWTVPYGRYFAGEHTAYPHGMVETAVSKALARAIKN 505

Best Local Similarity 41.8%; Pred. No. 1.4e-65; Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

Qy 3 LHVKWKLISVSVLITLYSYHT-VALSLKEHLADCLIEDKDYDTLQLTDNGLPHINTSHH 61  
 Db 6 LHL---LVLVPLSLISVSDWKAEQSQDPFEKCMODPDPYEQLLKXVWTGWNRNLKPQR 61  
 Qy 62 VVVGAGMAGLTAAKLLQDAGHTTILEANDRVRGVETYRNKEGYMAEMGAMRIPSSH 121  
 Db 62 VVVGAGVGLVAAKVLSDAHGKVTITLEADNRIGRIFTYRQNTGHTGEULGAMRMSSH 121  
 Qy 122 RIVQWFYKKGIVMNEPVMDDNTFTLVNGVRBTYVQENDDVLYKVNSEBEGKTSADD 181  
 Db 122 RILHKLCQGLNUNLTKEFDKNTWTEVHEYKLRLTVYVERKPEKLGALRPOEKGHSPED 181

Best Local Similarity 41.8%; Pred. No. 1.4e-65; Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

Qy 182 LLDRALOKVKVEEANCKAALEKYDVSKEYLKEGGGLSPGAVRMIDLUNEOUSMLYT 241  
 Db 182 IYQMLNQALDKDQKLUCKRKAMKKFERHTLLYLGLGNLSPAVQJGDYNSEDGFPYL 241

Best Local Similarity 41.8%; Pred. No. 1.4e-65; Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

Qy 242 ALSEMYYQDQWVNDMSVTYHEVTGGSOLLPPEARLSDVLPILLNSKVKHRSQDKGKVIVSY 301  
 Db 242 SPAELRAHSCSLDRQLYSRIVGGWDLIPRAILSLSGLVLLNAIVYAMTQSPHDVHVQI 301

Best Local Similarity 41.8%; Pred. No. 1.4e-65; Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

Qy 302 QTGNES-SLMDSADIVLVTTAKAALFIDFPDPLSLSKMEALRSVHYDSSTPKILLTERD 360  
 Db 302 ETSPPARNLKVLAQDVLTLTAGSPAVKRITFSPPPLPRHMQEALRLHYVPAVKFLSFRR 361

Best Local Similarity 41.8%; Pred. No. 1.4e-65; Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

Qy 361 KFWEDDGTRGGKSTTDGPGSRYIYYPHSHFTNETIGVLLASTWSDESSLFLUGASDEBLK 420  
 Db 362 PFWREEEHIEGGSNTDRPSRTFYP----EPREGA/LLASTWSDAAAFAGLSREBAL 416

Best Local Similarity 41.8%; Pred. No. 1.4e-65; Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

Qy 421 BLALRDLAKHG--EQWDKCTGIVVKKWKAADPYSIGAFAFLPTPYOHLEYAQELFSE- 476  
 Db 417 RLALDDVAALHGPPVRQLWDG-TGV-VKRWAEQDQSQGFFVWQP-----ALNOTEK 466

Best Local Similarity 41.8%; Pred. No. 1.4e-65; Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

Qy 477 -----GRVHFAGENTPHAVETETSMKSAIRATNN 508  
 Db 467 DDWTVPYGRYFAGEHTAYPHGMVETAVSKALARAIKN 505

## RESULT 5

US-10-16-087B-48  
 Sequence 48, Application US/10166087B  
 GENERAL INFORMATION:  
 APPLICANT: Ecopia Biosciences Inc.  
 APPLICANT: Farinet, Chris  
 APPLICANT: Stauffer, Alfredo  
 APPLICANT: Zazopoulos, Emmanuel  
 TITLE OF INVENTION: NUCLEIC ACID FRAGMENT ENCODING AN NRPs FOR THE BIOSYNTHESIS OF  
 TITLE OF INVENTION: ANTHRAMYCIN  
 FILE REFERENCE: 3014-ZUS  
 CURRENT APPLICATION NUMBER: US/10/166,087B  
 CURRENT FILING DATE: 2002-06-11  
 NUMBER OF SEQ ID NOS: 57  
 SOFTWARE: Patentin version 3.0  
 SEQ ID NO: 48  
 LENGTH: 478  
 TYPE: PRT  
 ORGANISM: Streptomyces refuineus subspecies thermotolerans  
 US-10-16-087B-48

Query Match 15.1%; Score 407; DB 6; Length 478;  
 Best Local Similarity 29.4%; Pred. No. 7.5e-22; Mismatches 83; Indels 70; Gaps 20;  
 Matche 144; Conservative 83; Mismatches 196; Indels 70; Gaps 20;  
 Qy 47 QTLNDGPHINTSHHVVTVGAGMAGTAALKLQDAGHTVTLANEDRVGGRVETYRN-E-K 105  
 Db 11 ETFDSGIPQHQGTSVUVGAGLAAAHBLTRQGVTVLEADSRRGGRTWTLREPFPA 70

Query Match 15.1%; Score 407; DB 6; Length 478;  
 Best Local Similarity 29.4%; Pred. No. 7.5e-22; Mismatches 83; Indels 70; Gaps 20;  
 Matche 144; Conservative 83; Mismatches 196; Indels 70; Gaps 20;  
 Qy 106 EGWYAMGAMTIPSSHRIVQMFVKLUGVENVNEFVMTDDNTTYLVNGVRERTYVQENPDV 165  
 Db 71 DGLRAEAGMTVTECHYTMHLYKENGIGTBDLVDTDFGYTHRNGVRIPPDVKGEHADL 130

Qy 166 LKVNSESEKGISADDLLRALQKVKEEYANGCKAA-----LEKYDRYSVKEYLK 216  
 Db 131 L--GLHPDPRHLTVEGMAARYVTEFNEKL---GPEIAQPVWAFTPRLDEVSVRVL 185

Qy 217 EGG----LSPGAVMRIGDLINNEQQLMAYTALESMIYDQADVNDSTV---YHEVTGGS 266  
 Db 186 ERGASAAAIGLMPEFLMRGGELESASAMANAR---YESGPRSFSSTAGAQWYKEGGT 241

Qy 267 DLIPEAFLSVLDVPTILNSKVKHROSPDGIVSYOTGENESSLMDLSADIVLVTTAKAA 326  
 Db 242 DMALARALLSRLGRBLRFLKPKVURIAQDDEAQTFL---DHGRJRTLCADRVVTAPFSM 299

Qy 327 LFDFD-PPLSLSKMEALRSVHDSSTSILLFRDKFW-----EDGIRGCKSIT-- 375  
 Db 300 RRYNLSMARSAAKHAARRRLRASYSTVFLQNRKREWPERRMLMSSTDATRTVDRDATPH 359

Qy 376 -DGPSPRYIYPSPHSFHNETIGVLLASVYTSDESLIFIGASDBELKELLRLAKI--HG 432  
 Db 360 LPQGPRTIV---ECWLTCG-----WQQAAM--SPEERYAYALNELEPLPGA 402

Qy 433 EQWWDKCTGVIVKWSAPPSLGAFAILTPYQ-HLEYAQUELFSSEGHRVHFAGENTAF-PH 490  
 Db 403 RENPELGTSV--AWDNPEPYAAGAYIL--PERGHSELMAATRAPEGRIHFAEHTAEPN 457

Qy 491 AW-JETSNKSAIR 502  
 Db 458 GGSMMNYALESSIR 470

RESULT 6  
 US-10-940-774A-11442  
 ; Sequence 11442, Application US/10940774A  
 ; GENERAL INFORMATION  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001307  
 ; CURRENT APPLICATION NUMBER: US/10/940.774A  
 ; CURRENT FILING DATE: 2004-09-15  
 ; PRIORITY APPLICATION NUMBER: 60/241,755  
 ; PRIORITY FILING DATE: 2000-10-20  
 ; PRIORITY APPLICATION NUMBER: 60/237,768  
 ; PRIORITY APPLICATION NUMBER: 60/231,498  
 ; PRIORITY FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 11442  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 US-10-940-774A-11442

Query Match Score 294; DB 6; Length 545;  
 Best Local Similarity 24.9%; Pred. No. 2.1e-13;  
 Matches 133; Conservative 86; Mismatches 176; Indels 140; Gaps 27;

Qy 51 NGPHINTSHHVVTVGAGMAGITAALKLQDAUGHTTILEANDRVRGVERTYRNEXEGWYA 110  
 Db 21 NGASAMSNKCDVUVGGGSGRAAKLHDSSLNVVLEADRVRGRTYTLRNQKVX-IV 79

Qy 111 EMGAMRI-PSSHRIQWFKKLGVF---MNEFVMTDDNTFYLVNGVRETTYVQO--- 161  
 Db 80 DUGGSYVQPTQRILR-LAKELGLETYKNEVER---LIHVVKGSXPFRGPFPVV 131

Qy 162 -NPDVLKVNVSSEKGKISSADDLL---RALQKVKEEVEANG-CKAAL-EKYDRYSVKE 213  
 Db 132 WNP--ITY-----LDHNNFWRTMDNGREIPSADPKAPLAEEWDNMTRME 175

Qy 214 YLREEGGSLSPGAVRMICDNLNEQSISYQDADNSVTS-YHEVT----- 263  
 Db 176 LL-----DKLCWTESKQL-ATLFVNLCVTAETHESALMFLWWYV 214

Qy 264 -----GGS DLLPPEAFSLVDVPIILNSKVKHROS DKGVIVSY 301  
 Db 215 KOCGGETTRIISTTNGGQERKTVGGSQVSBRIMDLJGDVKRPLRVIYDTRENVY-- 272

Qy 302 QTGNESLMDLSADIVLVTTAKAALFIDFDPLPLSKMEALRSVHYDSSTS KILLTRFRD 361  
 Db 273 ETLNHEM--YEAKVYVISAIPPTLGKMKIHFNPPMMRNOMITRVPLGSVTKCIVTYKEP 329

Qy 362 FWEDGUTRGKSITDGP SRYIY-----PSHSFTNETIGVLLASVYTSDESLFLIGAS 415  
 Db 330 FWRKDY-CGTMIIIDBEAPVAYTLDTRKREGNYAA--INGFILAHKARKLAR---TK 382

Qy 416 DEELKEL-----ALRDLAKINGEQVNDKCTGVIVKKWSADPSLGA PALFPTPYQHL 466  
 Db 383 EERLKLCLBLYAKVLSLEALEPVYEE-----KONCEQYSSGGCCYTYPGPGL 432

Qy 467 -EYAQELFSSGRHFAGEHTAEPH--AWIETSMKSAIRATNI---NKVANE 514  
 Db 433 TQYGRVLRQPVDRYIYAGTETA-TWMSGYMEGA EAGERAREILHAMGKIPEDB 486

RESULT 7  
 PCT-US05-09248-13  
 ; Sequence 13, Application PC/TUS0509248  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Xu, J.Janchao  
 ; TITLE OF INVENTION: DETECTION, ISOLATION AND USES OF RENALASE (MONOAMINE OXIDASE C)  
 ; FILE REFERENCE: 044574-5132-WO  
 ; CURRENT APPLICATION NUMBER: PCT/US05/09248  
 ; CURRENT FILING DATE: 2005-03-28  
 ; PRIOR APPLICATION NUMBER: US 60/554,552  
 ; PRIOR FILING DATE: 2004-03-19  
 ; PRIOR APPLICATION NUMBER: US 60/615,452  
 ; PRIOR FILING DATE: 2004-10-01  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: Patentin version 3.2  
 ; SEQ ID NO: 13  
 ; LENGTH: 520  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 PCT-US05-09248-13

Query Match Score 288; DB 1; Length 520;  
 Best Local Similarity 25.0%; Pred. No. 5.4e-13;  
 Matches 131; Conservative 84; Mismatches 169; Indels 140; Gaps 27;

Qy 62 VVIVGAGMAGTAALKLQDAUGHTTILEANDRVRGVERTYRNEXEGWYAEMGAMRI-PSS 120  
 Db 7 VVVVIGGIGSMMAAKLHDGLNVVLEADRVRGRTYTLRNQKVX-YVDLGGSYVGPTQ 65

Qy 121 HRIQWFKKLGVF---MNEFVMTDDNTFYLVNGVRETTYVQE---NPDVLKVNVS 171  
 Db 66 NRILR-LAKELGLETYKNEVER---LIHVVKGSXPFRGPFPWNP--ITY-- 112

Qy 172 ESEKGKISADDLL---RALQKVKEEVEANG-CKAAL-EKYDRYSVKE EGG LSPG 224  
 Db 113 -----LDHNNFWRTMDNGREIPSADPKAPLAEEWDNMTRME 152

Qy 225 AVRMMGDLINEQSISYQDADNSVTS-YHEVT----- 263  
 Db 153 -----DKLCWTESKQL-ATLFVNLCVTAETHESALMFLWWYV 153

Qy 264 -----GGS DLLPPEAFSLVDVPIILNSKVKHROS DKGVIVSYQTGNESLMDL 312  
 Db 201 TTNGGQERKTVGGSQVSBRIMDLJGDVKRPLRVIYDTRENVY--ETLNHEM--Y 255

Qy 313 SADIWLVTTAKAALFIDFDPLPLSKMEALRSVHYDSSTS KILLTRFRD 372  
 Db 256 EAKVYVISAIPPTLGKMKIHFNPPMMRNOMITRVPLGSVTKCIVTYKEPFWRKKDY-CGT 314  
 Qy 373 SITDGP SRYIY-----PSHSFTNETIGVLLASVYTSDESLFLIGASDEELKEL--- 422

Db 315 MIDGEA PAVAYTLLDDTTKPEGNYAA--IMGFILAHKARKLARL---TKEERLKKLCYL 368  
 Qy 423 ----ALRDLAKIHGEQWWDKCTGVIVKWWADPYSLAFALPTPYQHL-EYAQELFSE 476  
 Db 369 AKVLSLEALEPVHYYE-----KRNWCEBOYSGGCYTTFPRGLTQGRVLRQPV 418

Qy 477 GRVFAGENTTAPPH--AWIETSMKSAIRAATNI---NKVANEE 514  
 Db 419 DRIYFAGTETA-TWNSGYMEGAVEGIRAARILHAMGKIPDE 461

RESULT 9  
 PCT-US03-10870-448  
 ; Sequence 447, Application PC/TUS0310870  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mitokor, Inc.  
 ; BUCK INSTITUTE  
 ; APPLICANT: Buck Institute  
 ; GHOSH, Soumitra S.  
 ; APPLICANT: Ghosh, Soumitra S.  
 ; APPLICANT: Fahy, Boin D.  
 ; APPLICANT: Fahy, Bing  
 ; APPLICANT: Gibson, Bradford W.  
 ; APPLICANT: Gibson, Bradford W.  
 ; APPLICANT: Glenn, Gary M.  
 ; APPLICANT: Warnock, Dale E.  
 ; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION  
 ; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME  
 ; FILE REFERENCE: 660088-465PC  
 ; CURRENT APPLICATION NUMBER: PCT/US03/10870  
 ; CURRENT FILING DATE: 2003-04-04  
 ; NUMBER OF SEQ ID NOS: 3025  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 448  
 ; LENGTH: 520  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 PCT-US03-10870-448

Query Match 10.7%; Score 288; DB 1; Length 520;  
 Best Local Similarity 25.0%; Pred. No. 5.4e-13; Mismatches 84; Indels 140; Gaps 27;  
 Matches 131; Conservative 84; Mismatches 169; Indels 140; Gaps 27;

Qy 62 VVIVGAGMAGTAALKLQDAGHTVTLBEANDRIVGRVETYNBKEGRYAEANGAMRI-PSS 120  
 Db 7 VVVGGGISMGAALKLHDGLNVVLEARDRVGRTTYLNQVK-YVDLGGSYVGPTQ 65

Query Match 10.7%; Score 288; DB 1; Length 520;  
 Best Local Similarity 25.0%; Pred. No. 5.4e-13; Mismatches 84; Indels 140; Gaps 27;  
 Matches 131; Conservative 84; Mismatches 169; Indels 140; Gaps 27;

Qy 121 HRIVQWFVKLGVE--MNEFWMTDDMGREIPSADPKPLAEDWNNTMKELL----  
 Db 66 NRILR-LAKELEGETYKNEVER----LHHVKGSKYPRGPFPVWNP--ITY--- 112

Db 172 ESEKGISADDLD---RALQKVKEEVAANG-CKAAU-EKYDRYSYKEYLKEEGGLSPG 224

Qy 122 ESEKGISADDLD---LDBHNFWRTDDMGREIPSADPKPLAEDWNNTMKELL----  
 Db 66 NRILR-LAKELEGETYKNEVER----LHHVKGSKYPRGPFPVWNP--ITY--- 112

Qy 173 SADIVLVTTAKAALFIDDPPLSISKMEALRSVHYDSSTKILLFRDKFEDDGIRGGK 372

Db 113 SADIVLVTTAKAALFIDDPPLSISKMEALRSVHYDSSTKILLFRDKFEDDGIRGGK 372

Qy 123 SADIVLVTTAKAALFIDDPPLSISKMEALRSVHYDSSTKILLFRDKFEDDGIRGGK 372

Db 113 SADIVLVTTAKAALFIDDPPLSISKMEALRSVHYDSSTKILLFRDKFEDDGIRGGK 372

Qy 124 SADIVLVTTAKAALFIDDPPLSISKMEALRSVHYDSSTKILLFRDKFEDDGIRGGK 372

Db 113 SADIVLVTTAKAALFIDDPPLSISKMEALRSVHYDSSTKILLFRDKFEDDGIRGGK 372

Qy 125 EAKVYISAIPPLGMKIHNPPLPMNOMITRVLGSVICKIVYKEPFORKDY-CGT 314

Db 201 TTNGGOERKFVGGSGQYSERIMDLGDRVKLRPVIVIDQTRENVLY--ETLNHEM--Y 255

Qy 313 SADIVLVTTAKAALFIDDPPLSISKMEALRSVHYDSSTKILLFRDKFEDDGIRGGK 372

Db 153 SADIVLVTTAKAALFIDDPPLSISKMEALRSVHYDSSTKILLFRDKFEDDGIRGGK 372

Qy 256 EAKVYISAIPPLGMKIHNPPLPMNOMITRVLGSVICKIVYKEPFORKDY-CGT 314

Db 201 TTNGGOERKFVGGSGQYSERIMDLGDRVKLRPVIVIDQTRENVLY--ETLNHEM--Y 255

Qy 373 SITDGSRVYY----PSHSFHNTETIGVLLASLTSWSDESLFLGASDEBELKL--- 422

Db 315 MIDGEA PAVAYTLLDDTKPEGNYAA--IMGFILAHKARKLARL---TKEERLKKLCYL 368

Qy 256 EAKVYISAIPPLGMKIHNPPLPMNOMITRVLGSVICKIVYKEPFORKDY-CGT 314

Db 201 TTNGGOERKFVGGSGQYSERIMDLGDRVKLRPVIVIDQTRENVLY--ETLNHEM--Y 255

Qy 373 SITDGSRVYY----PSHSFHNTETIGVLLASLTSWSDESLFLGASDEBELKL--- 422

Db 315 MIDGEA PAVAYTLLDDTKPEGNYAA--IMGFILAHKARKLARL---TKEERLKKLCYL 368

Qy 423 ----ALRDLAKIHGEQWWDKCTGVIVKWWADPYSLAFALPTPYQHL-EYAQELFSE 476  
 Db 369 AKVLSLEALEPVHYYE-----KRNWCEBOYSGGCYTTFPRGLTQGRVLRQPV 418

Qy 477 GRVFAGENTTAPPH--AWIETSMKSAIRAATNI---NKVANEE 514  
 Db 419 DRIYFAGTETA-TWNSGYMEGAVEGIRAARILHAMGKIPDE 461

Db 369 AKVLSLEALEPVHYYE-----KRNWCEBOYSGGCYTTFPRGLTQGRVLRQPV 418

US-10-990-328A-8287							
Sequence ; Application US/10990328A							
GENERAL INFORMATION:							
APPLICANT: CARGILL, Michele							
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES USES THEROF							
FILE REFERENCE: CL001495							
CURRENT APPLICATION NUMBER: US/10/990, 328A							
CURRENT FILING DATE: 2004-11-17							
NUMBER OF SEQ ID NOS: 558824							
SOFTWARE: FastSEQ for Windows Version 4.0							
SEQ ID NO: 8287							
LENGTH: 520							
TYPE: PRT							
ORGANISM: Homo sapiens							
US-10-990-328A-8287							
Query Match Score 288; DB 6; Length 520;							
Best Local Similarity 25.0%; Pred. No. 5.4e-13; Gaps 27;							
Matches 131; Conservative 84; Mismatches 169; Indels 140; Gaps 27;							
Qy 62 VVIVGAGMUTAAKILQDAGHTVTILEANDRVGRVETYRNKEKGWYAEMGMARI-PSS 120							
Db 7 VVVGGAGMUTAAKILQDAGHTVTILEANDRVGRVETYRNKEKGWYAEMGMARI-PSS 120							
Qy 121 HRIVQWFKVKLGVE --MNEFVMTDDNTFVLYNGVRYTYYVQE ---NPDVLKVNVS 171							
Db 66 NRILR-LAKEGLGLETYKVNEVER----LHRRVGKSYSPFRGPFPVWNP--ITY--- 112							
Qy 172 ESEKGTSADDILD---RALQKVEEAVANG-CKAAL-EKYDRYSVKEYLBEGGLSPG 224							
Db 113 -----LDHNNNWRTMDDMGREIYSDAPWKAPLAEWDNMNTMKELL----- 152							
Qy 225 AVRIGDLINQEQLNQSLMYTALESEMIYDQADYNDSTV-----YHEVT----- 263							
Db 153 -----DKLCWTEASAKL-ATLFVNLCVTAETHESVSAIMELWTVRQCGGTTRIS 200							
Qy 264 -----GGSDLLPPEAFLSVLDPILLNSKVKHIBQSDKGIVVSYOTGNMESSLMDL 312							
Db 201 TTNGGQERFVGGSQVSERIMDLIGDRVKLERPVYIDQTRENVL--ETLNHEM---Y 255							
Qy 313 SADIIVVTTAKAALIDDFPPLSTSMEALRSVHDSTSSTKLILFRDKFWEDDGIRGSK 372							
Db 256 EAKYVVAISAIPTTLGMKTHNPPLPMRMQMTRIVPLGSVIKCVYKKEFWRKKDY-CGT 314							
Qy 373 SITDGPSRYYI-----PSHSFTHTNETCIVLAASYTWSDESSLFLGASDEELKEI---- 422							
Db 315 MIIDGEAPAYTLDKTPGNYAA--IMGFILAHARKJLAR---TKEBRURKLCLEY 368							
Qy 423 -----AIRDLAOKINGQEWWDKCTGVVKKNSADPYSIGALFTPYQHL-EYAQELFSSSE 476							
Db 369 AKVUGSLEALEPVYEE-----KWCCEQYSGGCCTYFPPGILTOYGRVLRQPV 418							
Qy 477 GRVFHAGEHTAFAFPH--AWIETSMGSAIRATNI---NFKVANEE 514							
Db 419 DRIYFGTETA-TWMSGYMEGAVERAGERAREILHAMGKIPDE 461							
RESULT 11							
US-10-990-328A-8288							
Sequence ; Application US/10990328A							
GENERAL INFORMATION:							
APPLICANT: CARGILL, Michele							
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES USES THEROF							
FILE REFERENCE: CL001495							
CURRENT APPLICATION NUMBER: US/10/990, 328A							
CURRENT FILING DATE: 2004-11-17							
NUMBER OF SEQ ID NOS: 558824							
SOFTWARE: FastSEQ for Windows Version 4.0							
SEQ ID NO: 8288							



Matches 121; Conservative 91; Mismatches 197; Indels 108; Gaps 18; Qy 62 VVIVGAGAGLTAALKLQDAGHTVTILEANPVRGGVRETYNEKEGYAENGAMRIPSSH 121 Db 16 VVVGGSIGSLSAAKLTTEYGVSVLVEARDRVGGRTTIRNEHDYDVGGAYGPTQN 75 Qy 122 RIVQWFVKLGIVEMNEFVMTDDNTFLYLNGVRETYVQE-----NP-DVLYKVNSE 174 Db 76 RIILR-LSKELGIETYKVNSE---RLVQYKGKTYPPRGAPPVWNPIAYLDN----125 Qy 175 KGISADDLDRALQKVKEVEANGCKAA--LEKYDRYSKEYLKEEGGLSPGAVRMIGDL 232 Db 126 -----NLWRTIDNMGEKEIPTDAPWEAQUADKWDKTMKBE-----L 160 Qy 233 LNEQSLMYTALSEMIVDQADYNDSVTYHEV-----263 Db 161 IDKICWTKTA-RRFAYLFVNINVTSPEHESALWFLWYKQCGGTTRIFSVTNGGQERKF 219 Qy 264 -GGSIDLPEAFPSVLDPILLNSKVKHROSDFKGIVYQTGNESSLMDLSADIYLVTT 322 Db 220 VGGSGQSERIMDLIGDQVKLNHPVTHDQSSDNIIIE-TLNHHEYECKYVINAAPPLT 278 Qy 323 AKAAFLFDPPPLSKMEALRSVYDSDTKILLFRDKFWEDDCIRGKKSITDOPSRYI 382 Db 279 AK---IHFRPELPAAERNQLIQRLLPGAVIKCMWYKEAFWKKKDYGCMIIDEDAPL- 333 Db 383 YPPSHSFHTNET-----IGVLLASYTWSDESLFLGASDEELKELAALRDL-AKIHG 432 Qy 384 -----SITLDDTKPDSLPAIMGFLARK-ADR---LAKLHKERIRKKICELAKVLG 382 Db 433 EQVWDKCTGVTVKRSADPYSLGAF-ALFTPYOHLEYAOELFSSGRVHPAGEHTA---487 Db 383 SQUEALPHVYEEKWNCEBQYSGCCTAYFPGIMTQYGRVTPQVGRIFFAGTETAKWS 442 Qy 488 -FPHAWIETSMKSARAATNINKVANEESTIEHTKDE 523 Db 443 GYMBSAVEAGERAAREVNLGLGKVTEKD1WQEPESK 479

Search completed: October 4, 2005, 13:57:37  
Job time : 81 secs

---

RESULT 15  
US-10-990-328A-8290  
; Sequence 8290, Application US/10990328A  
; GENERAL INFORMATION  
; APPLICANT: CARGILL, Michele  
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES  
; TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND  
; USES THEREOF  
; FILE REFERENCE: CL0101495  
; CURRENT APPLICATION NUMBER: US/10/990,328A  
; NUMBER OF SEQ ID NOS: 558824  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 8290  
; LENGTH: 527  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-10-990-328A-8290

Query Match 10.5%; Score 283; DB 6; Length 527;  
Best Local Similarity 23.4%; Pred. No. 1..3e-12;  
Matches 121; Conservative 91; Mismatches 197; Indels 108; Gaps 18;

Qy 62 VVIVGAGAGLTAALKLQDAGHTVTILEANPVRGGVRETYNEKEGYAENGAMRIPSSH 121 Db 16 VVVGGSIGSLSAAKLTTEYGVSVLVEARDRVGGRTTIRNEHDYDVGGAYGPTQN 75 Qy 122 RIVQWFVKLGIVEMNEFVMTDDNTFLYLNGVRETYVQE-----NP-DVLYKVNSE 174 Db 76 RIILR-LSKELGIETYKVNSE---RLVQYKGKTYPPRGAPPVWNPIAYLDN----125 Qy 175 KGISADDLDRALQKVKEVEANGCKAA--LEKYDRYSKEYLKEEGGLSPGAVRMIGDL 232 Db 126 -----NLWRTIDNMGEKEIPTDAPWEAQUADKWDKTMKBE-----L 160

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 4, 2005, 13:47:25 ; Search time 166 Seconds  
(without alignments)  
1220.858 Million cell updates/sec

Title: US-10-645-094-1  
Perfect score: 2703  
Sequence: 1 MNLHVKWKLSTVVLITY. .... TNINKVANEESTIHTKDEL 524

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

POST-processing: Minimum Match 0%  
Maximum Match 100%  
Listing First 4 summaries

Database : A\_Geneseq\_16Dec04:  
1: GeneseqP1980s:  
2: GeneseqP1990s:  
3: GeneseqP2000s:  
4: GeneseqP2001s:  
5: GeneseqP2002s:  
6: GeneseqP2003as:  
7: GeneseqP2003bs:  
8: GeneseqP2004s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2703	100.0	524	2	AAW96805	Aaw96805 An apopto
2	1048.5	38.8	523	8	AD06038	Ado6038 Mouse L-a
3	1034	38.3	630	5	ABB10103	Abb10103 Mouse imm
4	999	37.0	567	2	AAW75770	Aaw75770 Human oxi
5	999	37.0	567	2	AAY06480	Aay06480 Human tum
6	999	37.0	567	3	AAY99364	Aay99364 Human PRO
7	999	37.0	567	3	AAY93687	Aay93687 Amino aci
8	999	37.0	567	4	ABE66113	Aab66113 Protein o
9	999	37.0	567	4	AYY72874	Aay72874 Human PRO
10	999	37.0	567	4	AAB50962	Aab50962 Human PRO
11	999	37.0	567	4	AAU12409	Aau12409 Human PRO
12	999	37.0	567	5	ABB84904	Abb84904 Human PRO
13	999	37.0	567	5	ABB10104	Abb10104 Human imm
14	999	37.0	567	5	ABB95510	Abb95510 Human ang
15	999	37.0	567	6	AOB17853	Abo17853 Novel hum
16	999	37.0	567	6	ADA56835	Ada56835 Human sec
17	999	37.0	567	6	ABU81107	Abu81107 Human PRO
18	999	37.0	567	6	ABU71428	Abu71428 Human neo
19	999	37.0	567	6	ABU66807	Abu66807 Human PRO
20	999	37.0	567	6	ADA06866	Ada06866 Human sec
21	999	37.0	567	6	ABR47659	Abr47659 Human sec
22	999	37.0	567	6	ABU59888	Abu59888 Novel sec
23	999	37.0	567	6	ABG74758	Abg74758 Human PRO
24	999	37.0	567	6	ABO25078	Abo25078 Human sec
25	999	37.0	567	6	ABU67083	Abu67083 Human sec

## ALIGNMENTS

RESULT 1  
AAW96805 standard; protein; 524 AA.  
ID XX  
AC XX  
DT 23-APR-1999 (first entry)  
XX  
DE An apoptosis inducing protein.  
XX  
KW Cell death; apoptosis; inhibition; proliferation; cancer cell;  
KW apoptosis inducing protein; AIP; chub mackerel; anticancer.  
XX  
OS Scomber japonicus.  
XX  
PN W0952972-A1.  
XX  
PD 26-NOV-1998.  
XX  
PF 22-MAY-1998;  
XX  
PR 23-MAY-1997;  
XX  
PA (TENS-) TENSEI SUISAN CO LTD.  
PI Iwamoto M, Jung S;  
XX  
DR WPI; 1999-070139/06.  
N-PSDB; AAX15122.  
XX  
PF 22-MAY-1998;  
XX  
PR 23-MAY-1997;  
XX  
PA (TENS-) TENSEI SUISAN CO LTD.  
PI Iwamoto M, Jung S;  
XX  
DR WPI; 1999-070139/06.  
N-PSDB; AAX15122.  
XX  
PF 22-MAY-1998;  
XX  
PR 23-MAY-1997;  
XX  
PA (TENS-) TENSEI SUISAN CO LTD.  
PI Iwamoto M, Jung S;  
XX  
DR WPI; 1999-070139/06.  
N-PSDB; AAX15122.  
XX  
PF 22-MAY-1998;

The present sequence represents a protein which induces cell death (apoptosis) and inhibits the proliferation of cancer cells. The protein (apoptosis inducing protein, AIP) is isolated from chub mackerel. The protein can be used as an anticancer agent and as a reagent for study of the mechanisms of apoptosis in vitro. Sequence 524 AA;

Query Match 100.0%; Score 2703; DB 2; Length 524;  
Best Local Similarity 100.0%; Pred. No. 5.4e-206;  
Matches 524; Conservations 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNLHVVKWKLSTVVLITYTNINKVANEESTIHTKDELQDYLQLDNGLPHINTSH 60

Db	1 MNLVVKKLSSVLTLYSHTVALSKELHADLEDDYDTLQLTDNLGPHINTSH 60	CC amino acid oxidase having a fully defined amino acid sequence of 523 amino acids as given in the specification and L-amino acid oxidase activity. The invention may be useful for the production of compounds with an antibacterial activity. The invention is useful in preparing an ant-bacterial sterilisation composition as a hydrogen peroxide supply component. The invention is useful for preventing, treating bacterial infections such as sexually transmitted disease in the breast of livestock, for example mastitis, and provides an antimicrobial effect.
Qy	61 HVIIVGAGMAGTAAKLQDAGHTVILEANDRVRGVRVETYRNKEGWAEMGAMRISS 120	CC the present invention relates to a novel protein having 27-523 amino acids of L-amino acids as given in the specification and L-amino acid oxidase activity. The invention may be useful for the production of compounds with an antibacterial activity. The invention is useful in preparing an ant-bacterial sterilisation composition as a hydrogen peroxide supply component. The invention is useful for preventing, treating bacterial infections such as sexually transmitted disease in the breast of livestock, for example mastitis, and provides an antimicrobial effect.
Db	61 HVIIVGAGMAGTAAKLQDAGHTVILEANDRVRGVRVETYRNKEGWAEMGAMRISS 120	CC the present invention relates to a novel protein having 27-523 amino acids of L-amino acids as given in the specification and L-amino acid oxidase activity. The invention may be useful for the production of compounds with an antibacterial activity. The invention is useful in preparing an ant-bacterial sterilisation composition as a hydrogen peroxide supply component. The invention is useful for preventing, treating bacterial infections such as sexually transmitted disease in the breast of livestock, for example mastitis, and provides an antimicrobial effect.
Qy	121 HRIVOMFVKLGVMNEBFMDDNTFYLNGSYRETYVVOENPDVLKYNYESERKGISAD 180	CC the present sequence is that of the mouse L-amino acid oxidase protein of CC the present invention.
Db	121 HRIVOMFVKLGVMNEBFMDDNTFYLNGSYRETYVVOENPDVLKYNYESERKGISAD 180	CC the present sequence is that of the mouse L-amino acid oxidase protein of CC the present invention.
Qy	181 DLDRLAQKVKEEVEANGCKALEYDRYSYKEYLKEGGILSPGAVRMICDLNEQSAMY 240	XX
Db	181 DLDRLAQKVKEEVEANGCKALEYDRYSYKEYLKEGGILSPGAVRMICDLNEQSAMY 240	Sequence 523 AA;
Qy	241 TALESMYDQADVNDSVTYYHETVTGGSDLPLPAFLSVLDPILLNSKVKHIRQSDKGIVI 300	Query Match 38 8%; Score 1048.5; DB 8; Length 523;
Db	241 TALESMYDQADVNDSVTYYHETVTGGSDLPLPAFLSVLDPILLNSKVKHIRQSDKGIVI 300	Best Local Similarity 43 %; Pred. No. 1.9e-74; Mis matches 166; Indels 49; Gaps 7;
Qy	301 YQTGNBSSLMPLSADIVLVTTAKAALFDIDPPLSISKMEALRSVHYDSTSCKILLFRD 360	Matches 226; Conservative 79; Mi smatches 166; Indels 49; Gaps 7;
Db	301 YQTGNBSSLMPLSADIVLVTTAKAALFDIDPPLSISKMEALRSVHYDSTSCKILLFRD 360	Qy 27 LSLXKHLADCLDEDKDYDTLQLTDNLGLPHINTSHVAGMAGLTAAKLQDAGHTVT 86
Qy	361 KFWEDDGIRGGKSITDGPSPRYIYPSPHSFTNETIGVLLASYTNSDESLFLGASDEELK 420	Db 25 LALYENLVRCFCQDPYEAFLIAQNLHTSPLSKRVMVYGAAGLVAALKTLQDAGHEVT 84
Db	361 KFWEDDGIRGGKSITDGPSPRYIYPSPHSFTNETIGVLLASYTNSDESLFLGASDEELK 420	Qy 87 ILEANDRVRGVERVTRNEKEGWTAYMGMANRIPSSHRIIVONFVKLGVMNEBFMDDNTF 146
Qy	421 ELALRDIAKIHGEQWDKCTGVIVKWKSAUDPSLGAFAFLTPYQHLEYAEBLESSEGRVH 480	Db 85 ILEARNHIGGRVVTILRKERGWLPLGPRIPESHKLITYVQZGLKLNKFQDSNTW 144
Db	421 ELALRDIAKIHGEQWDKCTGVIVKWKSAUDPSLGAFAFLTPYQHLEYAEBLESSEGRVH 480	Qy 147 YLVNGVRETYVVOENPDVLKVNYESEKGISADIDLRLQKVKEEVEANGCKALEYK 206
Qy	481 PAGEHTAPPHAWIETSMKSAIRATAININKVANEESTIETHKDEL 524	Db 145 YLLNGQYRASEWMNPGLGIPRURSEKNTKVTFLFYQARTKVPHRKTSNCSSLSLY 204
Db	481 PAGEHTAPPHAWIETSMKSAIRATAININKVANEESTIETHKDEL 524	Db 207 DRYSKEYLKEGGILSPGAVRMICDLNEQSAMYTALEMSIYDQDNDVSVT - YHEVTG 264
Qy	524 PAGEHTAPPHAWIETSMKSAIRATAININKVANEESTIETHKDEL 524	Db 205 DSYSKAYLMKEGTLSKRAHR-----DGYNDENAGYTKSLLG 243
Db	524 PAGEHTAPPHAWIETSMKSAIRATAININKVANEESTIETHKDEL 524	Qy 265 GSD---LLPBAFL-----SVLDPILLNSKVKHIRQSDKGIVTYSQT- 303
Db	524 PAGEHTAPPHAWIETSMKSAIRATAININKVANEESTIETHKDEL 524	Db 244 VSEDCKHLLQKCP1FRDHRLWLCPIFNGLSASLKPTGKTCVRRVVRDGPVKVWYRTD 303
Qy	AC AD060382 standard: protein; 523 AA.	Qy 304 GNESSIMLDISADIVLVTTAKAALFDIDPPLSISKMEALRSVHYDSTSCKILLFRDKEW 363
AC	AC AD060382;	Db 304 GPTSLAHKLTDAYIAITASAKATLITFOPPLSRKTHALSVHYTSATRVLVCONERFW 363
DT	DT 15-JUL-2004 (first entry)	Qy 364 EDDGIRGGKSITDGPSPRYIYPSPHSFTNETIGVLLASYTNSDESLFLGASDEELKELA 423
DE	Mouse L-amino acid oxidase protein SegID2.	Db 364 EQDGI RGGSITDGPSPRYIYPSPHSFTNETIGVLLASYTNSDESLFLGASDEELKELA 423
XX	L-amino acid oxidase; antibacterial; antibacterial sterilisation;	Qy 424 LRDLAKITH--GEQWDKCTGVIVKWKSAUDPSLGAFAFLTPYQHLEYAEBLESSEGRVH 480
KW	hydrogen peroxide supply component; bacterial infection;	Db 422 LDLDLAVHRIPKKEELKRMCPKSAIKHWLDPLTGKTFPVQFDYSKQLSQEPGRIVY 481
KW	sexually transmitted disease; livestock; mastitis; antimicrobial; mouse;	Qy 481 PAGEHTAPPHAWIETSMKSAIRATAININKVANEESTIETHKDEL 524
Murine; enzyme.		Db 482 PAGEHTAPPHAWIETSMKSAIRATAININKVANEESTIETHKDEL 524
XX	OS Mus sp.	RESULT 3
PN	PN JP2004105119-A.	ID ABB10103
PD	PD 08-APR-2004.	ID ABB10103 standard; protein: 630 AA.
XX	XX PF 19-SEP-2002; 2002JP-00274082.	XX ABB10103;
PR	PR 19-SEP-2002; 2002JP-00274082.	XX DT 01-JUL-2002 (first entry)
XX	XX PA (SENT-) SENTAN KAGAKU GIJUTSU INCUBATION CENT KK.	XX DE Mouse immediate early interleukin-four induced protein.
XX	XX DR WPI: 2004-289536/27.	XX KW Interleukin-four induced protein; IL-4; cytostatic; antifungal; antiinflammatory; dermatological;
DR	DR N-PSDB; AD060381.	XX KW antibacterial immunomodulator; antiinflammatory; dermatological;
XX	XX XX AC	XX KW immunosuppressive; immune disease; tumour; fungal infection;
XX	XX PR 19-SEP-2002; 2002JP-00274082.	XX KW bacterial infection; systemic lupus erythematosus; inflammatory bowel disease; Guillain-Barre syndrome; Whipple's disease;
XX	XX PA (SENT-) SENTAN KAGAKU GIJUTSU INCUBATION CENT KK.	XX KW atopic dermatitis; food hypersensitivity; rheumatoid arthritis; osteoarthritis; diabetes mellitus; psoriasis; gene therapy; mouse.
XX	XX OS Mus sp.	XX

This invention relates to a novel protein having 27-523 amino acids of L-

Mus sp.

XX	WO200218574-A2.	Db	384 ARGEGS-----LLASITWSDAAPFAGLSDTQTLRLVLDG-RGV 437
PD	07-MAR-2002.	Qy	443 IVKWSADPYSLGAFALFTPIQHLEYAQELPSE-GRVHFACEHTAPHAWEETSMKSAI 501
XX	24-AUG-2001; 2001WO-US026462.	Db	438 -VKRAEDPHSQCGFVYQQPLVYGREADEYDNSAFAFGRIYPAGEHTALPHGWVETAVSGL 496
PF		Qy	502 RAATNIN 508
XX	25-AUG-2000; 2000US-0227818P.	Db	497 RAARVIN 503
PR			
XX	(NSHO-) NORTH SHORE-LONG ISLAND JEWISH RES.		
PA			
XX	Chu CC, Chavan SS, Mason JM;		
P1			
XX	WPI; 2002-329772/36.		
DR			
XX		RESULT 4	
		AAW75770	
		ID AAW75770 standard; Protein; 567 AA.	
		XX	
PT	New human immediate early interleukin-four (IL-4) induced protein and	AC AAW75770;	
PT	polynucleotides, useful for preventing or treating immune related	XX	
PT	disease, tumor, fungal or bacterial infection, e.g. lupus erythematosus	DT 21-DEC-1998 (first entry)	
PT	or Whipple's disease.	XX	
PS		DE Human oxidoreductase YTF03.	
XX		XX	
CC	The invention relates to an isolated polynucleotide, which encodes a	Disintegrin metalloproteinase; proteinase; BS10.55; human.	
CC	human immediate early interleukin-four (IL-4) induced protein. The	XX	
CC	activity of the polynucleotide of the invention may be described as,	OS Homo sapiens.	
CC	cytostatic, antifungal, antibacterial, immunomodulator, antiinflammatory,	XX	
CC	dermatological and immunosuppressive. The polynucleotide or antisense	Key Location/Qualifiers	
CC	oligonucleotide is useful for the manufacture of a medicament for	Peptide 1..22	
CC	preventing, treating or ameliorating a medical condition, particularly	/label= Sig_peptide	
CC	immune related disease, tumour, fungal infection or bacterial infection.	Peptide 21..44	
CC	The immediate early IL-4 induced protein is useful for the manufacture of	/note= "antigenic peptide"	
CC	a medicament for killing unwanted cells in a mammal. The antagonist is	Region 22	
CC	useful for the manufacture of a medicament for use in decreasing cell	/note= "a mitochondrial localisation motif is near Gln22"	
CC	death. The polynucleotide is also useful for diagnosing a pathological	Protein 23..567	
CC	condition, particularly an immune related disease. These diseases may	/label= Mat_protein	
CC	include systemic lupus erythematosus, inflammatory bowel disease,	Domain 62..78	
CC	Guillain-Barre syndrome, Whipple's disease, atop dermatitis, food	/note= "putative transmembrane domain"	
CC	hypersensitivity, rheumatoid arthritis, osteoarthritis, diabetes mellitus	Peptide 136..157	
CC	and psoriasis. The polynucleotide of the invention may be used in gene	/note= "antigenic peptide"	
CC	therapy. The current sequence represents the mouse immediate early	Peptide 171..189	
CC	interleukin-four induced protein	/note= "antigenic peptide"	
XX		272..289	
SQ	Sequence 630 AA;	/note= "putative transmembrane domain"	
		358..390	
Query	Query Match 38.3%; Score 1034; DB 5; Length 630;	/note= "antigenic peptide"	
Matches	Best Local Similarity 43.5%; Pred. No. 3.4e-73; Mismatches 100; Indels 12; Gaps 6;	Peptide 503..567	
Db	Matches 212; Conservative 100; Mismatches 163; Indels 12; Gaps 6;	/note= "antigenic peptide"	
Qy	26 ALSLKEHADCLIEDKDYLTLQLDNLPHINTSHHVIVAGGMAGTAKKLQDAGHTV 85	Peptide XX	
Db	25 AASSLNPIEKCMEDHDYBQLLKVVTLNRTSKPKQKVVVAGVAGVAAKMQLSDAGHV 84	Peptide XX	
Qy	86 TLEANDRVRGGVETYRNKEKGWYAEMGAMRIPSSHRIVQVFKVKGIVENNEFVMTDDNT 145	Peptide XX	
Db	85 TLEADNRIGGIFTFRDEKTWSWIGELGAMRMPSHSRILHKLCRTGLNLTOFTQYDENT 144	Peptide XX	
Qy	146 FVLNGVRERTVQENPDVLYKINSESEKGISADDLDRALQKVKEVBANGKALEK 205	Peptide XX	
Db	145 WTEVHNKLRLNVVEKPKLKGYNLRNRRGHSPEDITYQMALKNAFKDLKALGCKKAMN 204	Peptide PA	(SCHERING CORP.
Qy	206 YDRYSVKEYLKBEGGLSPGAVRMIGDILNEQSLMTASEMYDOADVNDSVTVEHTVGG 265	Peptide XX	Mueler CG, Lebecque SJB, Liu Y, Dowling LM, Huffine CF;
Db	205 FNKHTLLEYLLEBGNLSPAVQLLGDMSBEPFYLSFAEALRAHACSLDRLYSRVGG 264	Peptide PI	Gorman DM;
Qy	266 SDLPEAFPLSISKMEALSRYDSSTKILLTFRKFWEDDGIRGKSITDGPSPRVYIYP 385	Peptide XX	WPI; 1998-506353/43.
Db	265 WDLLPRLPLSSLSSGALLNAPVSIOTGRNDVRVHATLHSE-KTLLADVVLFLASGPA 323	Peptide DR	N-PSDB; AAV52605.
Qy	326 ALPIDFPPLSISKMEALSRYDSSTKILLTFRKFWEDDGIRGKSITDGPSPRVYIYP 385	Peptide XX	New isolated genes from human dendritic cells - which encode products having disintegrin-metallo-proteinase activities.
Db	324 LQRITESPLTRKRQBALRALHYVAASKVFLSFRRFWHEHIEGGHSNTDRPSLIFYP 383	Peptide XX	This is the amino acid sequence of human YTF03 protein, deduced from a dendritic cell cDNA sequence (see AAV52605). The YTF03 cDNA is distantly related to a family of enzymes which include monoamine oxidases, but the
Qy	386 SHSFHTNETIGVLLASYTWSDESLFLGASDEBLKELAQLDIAKHE -- QwwdkctgV 442	Peptide CC	CC

translation product does not have the key residues which covalently bind the FAD cofactor, and so may not exhibit monoamine oxidase activity. The cellular types which express messages encoding YTF03 suggest that signals important in cell differentiation and development are mediated by them. The invention provides a process for recombinant production of YTF03, host cells, expression vectors and specific antibodies. The products can be used for detection, diagnosis, development of therapeutic methods and drug screening

XX Sequence 567 AA;

Query Match Score 999; DB 2; Length 567;  
Best Local Similarity 41.8%; Pred. No. 1.8e-70;  
Matches 217; Conservative 99; Mismatches 1/1; Indels 32; Gaps 9;

Qy 3 LHIVKWKSLSVVSLITYSHT-VALSKEHLAIDCLEKDYDTLLQLQDGLPHINTSHH 61  
Db 6 LHL---LVLVPILSLVASQDMKAERQDPPFKCMQDPDXEQLLKVKVTWGLNRTLKPQR 61

Qy 62 VVIVGAGMAGLTAAKLQDAGHTVILEANDRVRGVETVNEKEGYAEMGAMRILPSH 121  
Db 62 VVIVGAGTAGLVBAKVLSDAGHKRVTLDEADNRVGRGVETVNEKEGYAEMGAMRILPSH 121

Qy 122 RIVQWFVKKLGKEMNEFWMTDDNTFVLYNGVRERTYQQENPDVLYKVNSESEKGISADD 181  
Db 122 RILHKLCQGLGNLNUKTFTQYDQNTWTETHEVKLNRYVVEKPEKLGYLARPOEKGHSPED 181

Qy 182 LLDRALQKVKEEANGCKAALEKYDVSYKEYLKEGGGLSPGAIVRMGDLIINEQSILMYT 241  
Db 182 IYOMALNQALKDJKALGGRKAMKFKFHITLLEYLGLGNGNSRPDVGDMSEDGFFYL 241

Qy 242 ALSEMIIYDOADYNDSVTYTHEVTGGSIDLLEPAEFLSVDLPIILNSKVKHRSODKGIVTSY 301  
Db 242 SFAEALRHSCLSDRLOYSRIVGWDUPLRALLSSLGVLINAPVATMGTGPHDTHVQI 301

Qy 302 QTGNES-SLMDSADIVVTTAKAALFIDPDPPLSTSMEALRSVHDSTSKILLFRD 360  
Db 302 ETPSPPARNLKVKLADVVLTAGPAVKRITSPPLRHMQEAIRRHYPATKVFLSPRR 361

Qy 361 KFWDDGKLRGGKSITDGSRVYIYPPSHSFHTNETIGVILASYTWSDESLIFGASDEELK 420  
Db 362 PFWREEHIEGGHSNTDPRSMIFYP----PPREGAILLASYTWSAAAAPAGLSREAL 416

Qy 421 ELALRDLIAKHG--EQWDKCTGTVIYKWKWSDPYSIGAFALPTPKQHLEYAQELFSSE- 476  
Db 417 RLALDDVAALHPGVVROWDG-TGV-TKWAIDQHESCGFVQQP-----ALWQTEK 466

Qy 477 -----GRVHAGENTAPPHWMIETMSKSAIRAAVIN 508  
Db 467 DDWTVPGYRIPYFAGENTAPPHWMIETMSKSAIRAAVIN 505

RESULT 5  
AY06480 standard; protein; 567 AA.  
XX AC AAY06480;  
XX DT 27-SEP-1999 (First entry)  
XX DB Human tumour-associated protein PRO1265.  
XX KW PRO1265; UNQ636; cancer; tumour; diagnosis; therapy; human.  
XX OS Homo sapiens.  
XX FH Location/Qualifiers  
1..21 /note= "signal peptide"  
Protein /note= "mature protein"  
FT Modified-site 54..57 /note= "Asn is N-glycosylated"  
FT

PT Region 61..80 "homology to D-amino acid oxidase"  
FT FT  
FT Modified-site 134..137 /note= "Asn is N-glycosylated"  
FT FT  
FT Modified-site 220..223 /note= "Asn is N-glycosylated"  
FT FT  
FT Modified-site 559..562 /note= "Asn is N-glycosylated"  
XX XX  
PN WO995170-A2.  
XX XX  
PD 15-JUL-1999.  
XX XX  
PF 05-JAN-1999; 99WO-US000106.  
XX PR 05-JAN-1998; 98US-0070440P.  
PR 29-APR-1998; 98US-008500P.  
PR 22-MAY-1998; 98US-008414P.  
PR 10-JUN-1998; 98US-008442P.  
PR 10-NOV-1998; 98US-0101783P.  
PR 20-NOV-1998; 98US-0103904P.  
PA (GETH ) GENENTECH INC.  
Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA, Roy MA;  
Wood WI;  
WPI; 1999-430385/36.  
DR N-PSDB; AAX8757.  
XX  
Antibody against proteins expressed in neoplastic cells, useful for tumor diagnosis and treatment.  
Example 1; Fig 8; 162pp; English.  
This sequence represents human PRO1265 (UNQ636), a 62.9 kDa protein (pi 8.9) encoded by the novel cDNA clone DNA6064 (see AAX87257). Amplification of DNA6074 occurs in various lung and colon tumours and cell lines, suggesting a significant role in tumour formation and growth. Antagonists (e.g. antibodies) directed to PRO1265 may have use in cancer therapy. The invention identifies 14 genes (see AAX87254-67) that are amplified in the genome of tumour cells. Such amplification is expected to be associated with overexpression of the gene product and to contribute to tumorigenesis. The encoded proteins (see AAY06477-90) may be useful targets for the diagnosis and/or treatment (including prevention) of certain cancers, and may act as predictors of the prognosis of tumour treatment. Antibodies that bind the proteins are claimed and used in claimed cancer diagnostic kits  
Sequence 567 AA;  
Query Match 37.0%; Score 999; DB 2; Length 567;  
Best Local Similarity 41.8%; Pred. No. 1.8e-70;  
Matches 217; Conservative 99; Mismatches 1/1; Indels 32; Gaps 9;  
Qy 3 LHIVKWKSLSVVSLITYSHT-VALSKEHLAIDCLEKDYDTLLQLQDGLPHINTSHH 61  
Db 6 LHL---LVLVPILSLVASQDMKAERQDPPFKCMQDPDXEQLLKVKVTWGLNRTLKPQR 61  
Qy 62 VVIVGAGMAGLTAAKLQDAGHTVILEANDRVRGVETVNEKEGYAEMGAMRILPSH 121  
Db 62 VVIVGAGTAGLVBAKVLSDAGHKRVTLDEADNRVGRGVETVNEKEGYAEMGAMRILPSH 121  
Qy 122 RIVQWFVKKLGKEMNEFWMTDDNTFVLYNGVRERTYQQENPDVLYKVNSESEKGISADD 181  
Db 122 RILHKLCQGLGNLNUKTFTQYDQNTWTETHEVKLNRYVVEKPEKLGYLARPOEKGHSPED 181  
Qy 182 IYOMALNQALKDJKALGGRKAMKFKFHITLLEYLGLGNGNSRPDVGDMSEDGFFYL 241  
Db 182 IVVVGAGVAGLVAARKVLSDAHGKVITLEADNRIGRIFTYRDQNTGWIGELGMAMRMPSSH 121  
Qy 242 ALSEMIIYDOADYNDSVTYTHEVTGGSIDLLEPAEFLSVDLPIILNSKVKHRSODKGIVTSY 301  
Db 242 SFAEALRHSCLSDRLOYSRIVGWDUPLRALLSSLGVLINAPVATMGTGPHDTHVQI 301  
Qy 302 QTGNES-SLMDSADIVVTTAKAALFIDPDPPLSTSMEALRSVHDSTSKILLFRD 360  
Db 302 ETPSPPARNLKVKLADVVLTAGPAVKRITSPPLRHMQEAIRRHYPATKVFLSPRR 361  
Qy 361 KFWDDGKLRGGKSITDGSRVYIYPPSHSFHTNETIGVILASYTWSDESLIFGASDEELK 420  
Db 362 PFWREEHIEGGHSNTDPRSMIFYP----PPREGAILLASYTWSAAAAPAGLSREAL 416  
Qy 421 ELALRDLIAKHG--EQWDKCTGTVIYKWKWSDPYSIGAFALPTPKQHLEYAQELFSSE- 476  
Db 417 RLALDDVAALHPGVVROWDG-TGV-TKWAIDQHESCGFVQQP-----ALWQTEK 466  
Qy 477 -----GRVHAGENTAPPHWMIETMSKSAIRAAVIN 508  
Db 467 DDWTVPGYRIPYFAGENTAPPHWMIETMSKSAIRAAVIN 505





IPS	Claim 61; Fig 8; 220pp; English.	XX	PP	18-FEB-2000;	2000WO-US004342.
CC	The present sequence represents a novel human polypeptide. The specification describes novel polypeptides designated PRO201, PRO292, PRO327, PRO344, PRO343, PRO347, PRO357, PRO715, PRO1017, PRO112, PRO125, PRO509, PRO853 and PRO882. These genes are amplified in the genome of tumour cells. The polypeptides are believed to contribute to tumourigenesis. The polypeptides are useful target for the identification of certain cancers, and may act as predictors of the prognosis of tumour treatment. Antibodies against these polypeptides are useful in the treatment and diagnosis of neoplastic cell growth and proliferation in mammals	XX	PR	23-JUN-1999;	99US-0141037P.
CC		XX	PR	20-JUL-1999;	99US-0144158P.
CC		XX	PR	01-SEP-1999;	99US-014568P.
CC		XX	PR	29-OCT-1999;	99WO-US020111.
CC		XX	PR	30-NOV-1999;	99US-0162506P.
CC		XX	PR	02-DEC-1999;	99WO-US028313.
CC		XX	PR	02-DEC-1999;	99WO-US02851.
CC		XX	PR	16-DEC-1999;	99WO-US030095.
CC		XX	PR	05-JAN-2000;	2000WO-US00219.
CC		XX	PR	06-JAN-2000;	2000WO-US00376.
XX	Sequence 567 AA;	XX	PA	(GETH ) GENENTECH INC.	
Query Match	37.0%; Score 999; DB 3; Length 567;	XX	PA		
Best Local Similarity	41.8%; Pred. No. 1. 8e-70;	XX	PI	Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S, Gao W, Goddard A, Grimaldi CJ, Gurney AL, Hillian KJ, Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Thomas D, Williams PM, Wood WI;	
Matches 211; Conservative	99; Mismatches 171; Indels 32; Gaps 9;	XX	PI	Watanabe CK;	
DY	3 LHVVWKLSVVSLTLYSHT-VALSKEHLADCLEDKDYDTLQLTLGLPHINTSHH 61	XX	PI		
Db	6 LHL---LVLPVLISLVSQDWKAERSODPEFEKCMODPYEQUKVTVWGLNRLTKPQR 61	XX	DR	WPI; 2001-071395/08.	
DY	62 VVYGAGAGLITAKLQLQAGHTVILEANDRYSGRVEYTRNEREGWYAMGARIPTSH 121	XX	XX	Secreted and transmembrane proteins and nucleic acids designated PRO, PT useful as hybridization probes, in chromosome and gene mapping and gene therapy.	
Db	62 VVYGAGAGLVAALKVLSAGHKVTVILEADNRIGRIFTYRDQNTGWICELGAMRMPSSH 121	XX	XX	Claim 1; Fig 50; 707pp; English.	
DY	122 RIVQFWVKLGVENNEFVNTDDNTFYLNGVRERTYYQENPDVLYKNTNSEKGSADD 181	XX	XX	Claim 1; Fig 50; 707pp; English.	
Db	122 RILHKLCKQGLLNJKTFQDNTWTEEVKEVLKNYVVKPERGLYARQPQEGHSPBD 181	XX	CC	The present invention relates to secreted and transmembrane proteins.	
DY	182 LLDRALQKVEKEYANGCAALEKYDYSKEYLKEEGGLSPGAVRMTCDLINBOSLMYT 241	XX	CC	These proteins and the DNA encoding them may be used as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. They may also be used to generate either	
Db	182 IYQMLAQNLQALKDILKALGCKKAMKKPERHTILEYLGEGNLSRPAVQLGDMSEDFPFL 241	XX	CC	transgenic animals or knockout animals which are in turn useful for development and screening of therapeutically useful reagents. The nucleic acids may also be used in gene therapy.	
DY	242 ALSEMYDQADVDTSVTHBVITGESSDLLEBAFSLVLLSRVKRHRQSDGKVIVY 301	XX	CC	Claim 1; Fig 50; 707pp; English.	
Db	242 SFAEALRAHSCLSDRLQYSRIVCGWDLLPRAALLSSLGVLVLLAPVAVANTQGPHDVAVQI 301	XX	XX	Sequence 567 AA;	
DY	302 QTGNES-SMIDLSDASDIVVTTTAKAALFIDFDPPPLSISKMEALRSVHYSSTSKILLTFRD 360	XX	Query Match	37.0%; Score 999; DB 4; Length 567;	
Db	302 ETSPPARNPKVLRVLLTASGPVKRITFSPPLRHMQLRHLHYPATVFLSFR 361	XX	Best Local Similarity	41.8%; Pred. No. 1.8e-70;	
DY	361 KEWEDDGIRGGKSITDGPSERYIYPSPHSSPTNPIGVLLASITYMSDESLIFGLASDEEK 420	XX	Matches	91; Mismatches 171; Indels 32;	
Db	362 PFPREEHGGHSNTDRPMIFP-----PPREGALLIASITYMSDAAAFAGLSREEA 416	XX	GapS	9	
DY	421 ELALRDLAKING---EQWDWKCTCVIKRWSADYSLGFAFLFTPYQHLEYAOPLFSSS- 476	XX	Qy	3 LHVVWKLSVVSLTLYSHT-VALSKEHLADCLEDKDYDTLQLTLGLPHINTSHH 61	
Db	417 RLALDDVAALHGPVYRQLWDG-TGV-VKRAWEAOHSQGFVVQPP-----ALWQTEK 466	XX	Db	6 LHL---LVLPVLISLVSQDWKAERSODPEFEKCMODPYEQUKVTVWGLNRLTKPQR 61	
DY	477 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Qy	62 VVYGAGAGLITAKLQLQAGHTVILEANDRYSGRVEYTRNEREGWYAMGARIPTSH 121	
Db	467 DDWTVPYGRIFYFAGEHTAYPHGMWETAVSRLRAAIKIN 505	XX	Db	62 VVYGAGAGLVAALKVLSAGHKVTVILEADNRIGRIFTYRDQNTGWICELGAMRMPSSH 121	
DY	478 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Qy	122 RIVQFWVKLGVENNEFVNTDDNTFYLNGVRERTYYQENPDVLYKNTNSEKGSADD 181	
Db	478 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	122 RILHKLCKQGLLNJKTFQDNTWTEEVKEVLKNYVVKPERGLYARQPQEGHSPBD 181	
DY	479 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Qy	182 LLDRALQKVEKEYANGCAALEKYDYSKEYLKEEGGLSPGAVRMTCDLINBOSLMYT 241	
Db	479 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	182 SFAEALRAHSCLSDRLQYSRIVCGWDLLPRAALLSSLGVLVLLAPVAVANTQGPHDVAVQI 301	
DY	480 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Qy	302 QTGNES-SMIDLSDASDIVVTTTAKAALFIDFDPPPLSISKMEALRSVHYSSTSKILLTFRD 360	
Db	480 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	302 ETSPARNPKVLRVLLTASGPVKRITFSPPLRHMQLRHLHYPATVFLSFR 361	
DY	481 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Qy	361 KEWEDDGIRGGKSITDGPSERYIYPSPHSSPTNPIGVLLASITYMSDESLIFGLASDEEK 420	
Db	481 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	362 PFWREHIEGHSNTDRPMIFP-----PPREGALLIASITYMSDAAAFAGLSREEA 416	
DY	482 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Qy	421 ELALRDLAKING---EQWDWKCTCVIKRWSADYSLGFAFLFTPYQHLEYAOPLFSSS- 476	
Db	482 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	421 ELALRDLAKING---EQWDWKCTCVIKRWSADYSLGFAFLFTPYQHLEYAOPLFSSS- 476	
DY	483 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Qy	478 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
Db	483 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	478 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
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DY	485 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Qy	480 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
Db	485 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	481 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
DY	486 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Qy	481 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
Db	486 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	482 PFWREHIEGHSNTDRPMIFP-----PPREGALLIASITYMSDAAAFAGLSREEA 416	
DY	487 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Qy	482 PFWREHIEGHSNTDRPMIFP-----PPREGALLIASITYMSDAAAFAGLSREEA 416	
Db	487 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	483 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
DY	488 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Qy	483 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
Db	488 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	484 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
DY	489 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Qy	484 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
Db	489 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	485 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
DY	490 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Qy	485 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
Db	490 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	486 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
DY	491 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Qy	486 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
Db	491 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	487 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
DY	492 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Qy	487 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
Db	492 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	488 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
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Db	496 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	492 PFWREHIEGHSNTDRPMIFP-----PPREGALLIASITYMSDAAAFAGLSREEA 416	
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Db	497 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	493 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
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Db	500 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	496 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
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Db	501 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	497 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
DY	502 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Qy	497 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
Db	502 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	498 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
DY	503 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Qy	498 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
Db	503 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	499 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
DY	504 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Qy	499 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
Db	504 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	500 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
DY	505 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Qy	500 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
Db	505 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	501 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
DY	506 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Qy	501 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
Db	506 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	502 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
DY	507 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Qy	502 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
Db	507 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	503 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
DY	508 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Qy	503 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
Db	508 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	504 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
DY	509 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Qy	504 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
Db	509 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	505 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
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Db	510 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	506 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
DY	511 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Qy	506 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
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Db	512 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	508 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
DY	513 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Qy	508 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
Db	513 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	509 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
DY	514 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Qy	509 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
Db	514 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	510 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
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Db	515 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	511 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
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Db	516 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	512 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
DY	517 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Qy	512 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
Db	517 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	513 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
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Db	518 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	514 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
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Db	520 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	521 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
DY	521 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Qy	521 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
Db	521 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	522 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
DY	522 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Qy	522 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
Db	522 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	523 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
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Db	523 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	524 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
DY	524 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Qy	524 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
Db	524 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	525 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
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Db	525 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	526 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
DY	526 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Qy	526 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
Db	526 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Db	527 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
DY	527 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	XX	Qy	527 -----GRHVFAGEHTAHPHANTEETSMKSAIRATIN 508	
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Db 417 RLADDVAALHGPVVRQLWDG-TGV-VKRWAAEDQHSQGFFVVQQPP-----ALWQTEK 466  
 PR 31-AUG-1999; 99US-0151733P.  
 PR 01-BEP-1999; 99WO-US00111.  
 PR 16-DEC-1999; 99NO-US00095.  
 PR 18-FEB-2000; 2000WO-US001342.  
 PR 01-MAR-2000; 2000WO-US005601.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 17-MAY-2000; 2000WO-US03705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 05-JUN-2000; 2000US-0209832P.  
 XX PA (GETH ) GENENTECH INC.  
 XX PI Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Tumas D;  
 XX PI Watanabe CK, Wood WI;  
 XX DR WPI; 2001-226590/23.  
 XX DR N-PSPDB; AAD02320.  
 PT New PRO polypeptides for treating immune related and inflammatory diseases such as rheumatoid arthritis, systemic vasculitis, asthma, antiinflammatory; dermatological; immunosuppressive; antirheumatic; antiarthritic; osteopathic; antihaemostatic; antidiabetic; antiviral; antipsoriatic; antiallergic; antiarthrathropathy; systemic sclerosis; systemic lupus erythematosis; sarcoidosis; idiopathic inflammatory myopathy; Sjogren's syndrome; spondylarthropathy; systemic sclerosis; sclerosing cholangitis; autoimmune thymocytopenia; Guillain-Barre syndrome; Whipple's disease; demyelinating polyneuropathy; Guillain-Barre syndrome; inflammatory bowel disease; glutamyl-sensitive enteropathy; skin disease; allergic rhinitis; atopic dermatitis; food hypersensitivity; urticaria; eosinophilic pneumonia; hypersensitivity pneumonitis; graft rejection; idiopathic pulmonary fibrosis; graft-versus-host-disease.  
 OS XX  
 CC The present sequence is PRO1265 protein encoded by DNA60764-1533 cDNA clone. The PRO protein, its agonist or antagonist or its antibody which are capable of enhancing or inhibiting the proliferation of T-lymphocytes or autoimmune hemolytic anaemia, and diabetes mellitus.  
 PS XX  
 PS Claim 10; Fig 2; 118pp; English.  
 CC The present sequence is PRO1265 protein encoded by DNA60764-1533 cDNA clone. PRO protein, its agonist or antagonist or its antibody which are capable of enhancing or inhibiting the proliferation of T-lymphocytes or autoimmune hemolytic anaemia, and diabetes mellitus.  
 CC XX  
 CC The present sequence is PRO1265 protein encoded by DNA60764-1533 cDNA clone. The PRO protein is useful for treating systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondylarthropathy, systemic sclerosis, idiopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demelinating disease of the central or peripheral nervous system, chronic idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, chronic inflammatory demyelinating polyneuropathy, hepatobiliary disease, infectious or autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's disease, autoimmune or immune-mediated skin diseases such as bullous skin disease, erythema multiforme and contact dermatitis, psoriasis, allergic diseases such as asthma, allergic rhinitis, atopc dermatitis, food hypersensitivity and urticaria, immunologic diseases of the lung such as eosinophilic pneumonias, idiopathic pulmonary fibrosis, hyper-sensitivity pneumonitis, transplantation associated diseases such as graft rejection or graft-versus-host-disease.  
 CC XX  
 SQ Sequence 567 AA;  
 Query Match 37.0%; Score 999; DB 4; Length 567;  
 Best Local Similarity 41.8%; Pred. No. 1..8e-70;  
 Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;  
 LHL----IVLVPIPLSLVASDQWKAERSQDPFEKCKMDQDPYEQOLJKVVTWLNRTLKPOR 61  
 3 LHVKWKLSVSVLTLVYSHT-VALSLKEHLADCLEKDYDTLQLTDNLGLPHNTSHH 61  
 VVIVAGMAGITAAKLQDAGHTVILEANDRGGFVETYRNKEBQWYAENGAMRIPSSH 62  
 62 VVIVAGGAGVGLVAATYLDAGHKOTITLEADNRIGRIFTYRDQNTGWIGELGAMRMPSHH 121  
 RIVQFVKKLGVEMNEFVMTDDNTFLYLVNGVRYRTVVOENPDVLYKVNVSSEKGISADD 181  
 62 RILHKUCQGLNLTKFTQIDKNTVVEKPEKGYALRPQEKGHSPEED 181  
 122 LLDRALQKVKEEVEANGKAALEKVDYRSKEYLKEBEGGSPGAVRMIGDLNNEQSLMYT 241  
 122 IYQMALNQALKDLKALGCRKAMKKPRHTLLEYLGEGNISRPAVQLLGDYMSEDGFFYL 241  
 182 ALSEMIVYDQADVNDSVTYHEVTGGSDLPEAFLSVLDVPILLSSKVYHIROSDKGVIVSY 301  
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Db 417 RLADDVAALHGPVVRQLWDG-TGV-VKRWAAEDQHSQGFFVVQQPP-----ALWQTEK 466  
 QY 477 -----GRVHFAGEHTTAAPHWAIETMSKSAIRAAINTN 508  
 PR 01-BEP-1999; 99WO-US00111.  
 PR 16-DEC-1999; 99NO-US00095.  
 PR 18-FEB-2000; 2000WO-US001342.  
 PR 01-MAR-2000; 2000WO-US005601.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 17-MAY-2000; 2000WO-US03705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 05-JUN-2000; 2000US-0209832P.  
 XX PA (GETH ) GENENTECH INC.  
 XX PI Goddard A, Godowski PJ, Gurney AL, Hillan KJ, Tumas D;  
 XX PI Watanabe CK, Wood WI;  
 XX DR WPI; 2001-226590/23.  
 XX DR N-PSPDB; AAD02320.  
 PT New PRO polypeptides for treating immune related and inflammatory diseases such as rheumatoid arthritis, systemic vasculitis, asthma, antiinflammatory; dermatological; immunosuppressive; antirheumatic; antiarthritic; osteopathic; antihaemostatic; antidiabetic; antiviral; antipsoriatic; antiallergic; antiarthrathropathy; systemic sclerosis; systemic lupus erythematosis; sarcoidosis; idiopathic inflammatory myopathy; Sjogren's syndrome; spondylarthropathy; systemic sclerosis; sclerosing cholangitis; autoimmune thymocytopenia; Guillain-Barre syndrome; Whipple's disease; demyelinating polyneuropathy; Guillain-Barre syndrome; chronic inflammatory bowel disease; glutamyl-sensitive enteropathy, Whipple's disease, allergic rhinitis; atopic dermatitis; food hypersensitivity; urticaria; eosinophilic pneumonia; hypersensitivity pneumonitis; graft rejection; idiopathic pulmonary fibrosis; graft-versus-host-disease.  
 OS XX  
 CC The present sequence is PRO1265 protein encoded by DNA60764-1533 cDNA clone. The PRO protein, its agonist or antagonist or its antibody which are capable of enhancing or inhibiting the proliferation of T-lymphocytes or autoimmune hemolytic anaemia, and diabetes mellitus.  
 PS XX  
 PS Claim 10; Fig 2; 118pp; English.  
 CC The present sequence is PRO1265 protein encoded by DNA60764-1533 cDNA clone. The PRO protein is useful for treating systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondylarthropathy, systemic sclerosis, idiopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demelinating disease of the central or peripheral nervous system, chronic idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, chronic inflammatory demyelinating polyneuropathy, hepatobiliary disease, infectious or autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's disease, autoimmune or immune-mediated skin diseases such as bullous skin disease, erythema multiforme and contact dermatitis, psoriasis, allergic diseases such as asthma, allergic rhinitis, atopc dermatitis, food hypersensitivity and urticaria, immunologic diseases of the lung such as eosinophilic pneumonias, idiopathic pulmonary fibrosis, hyper-sensitivity pneumonitis, transplantation associated diseases such as graft rejection or graft-versus-host-disease.  
 CC XX  
 SQ Sequence 567 AA;  
 Key Location/Qualifiers  
 FH 1..21  
 FT /label= Signal\_peptide  
 FT 22..567  
 Protein /label= Mature\_human\_PRO1265\_protein  
 FT 35..43  
 Modifid-site /label= Tyrosine\_kinase\_phosphorylation\_site  
 FT 52..58  
 FT /note= "N-myristoylation site"  
 FT 54..58  
 FT /note= "Asn is N-glycosylated"  
 Region FT 61..81  
 FT /label= D-amino\_acid\_oxidase\_protein  
 FT 66..74  
 FT /note= "N-myristoylation site"  
 FT 71..77  
 FT /note= "N-myristoylation site"  
 FT 130..136  
 FT /note= "N-myristoylation site"  
 FT 132..138  
 FT /note= "N-myristoylation site"  
 FT 134..138  
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 FT /label= Tyrosine\_kinase\_phosphorylation\_site  
 FT 198..204  
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 FT 220..224  
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 FT 595..600  
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 FT 601..606  
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 FT 607..612  
 FT /note= "Asn is N-glycosylated"  
 FT 613..619  
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 Db 362 PFWREHLEGGHENTDSSRMIFYP---PPNEGALLASYTWSDAAAAGLSSREAL 416  
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 Db 467 DDWTVPYGRYFAGEHTAYPHGMVETAVSKSALARAIKIN 505

## RESULT 10

AAB50962  
 ID AAB50962 standard; protein; 567 AA.  
 XX  
 AC AAB50962;  
 XX  
 DT 21-MAR-2001 (first entry)

Human PRO1265 protein.

Human: PRO; cytostatic; neuroprotective; respiratory general;  
 KW antiangiogenic; immunosuppressive; immunobiulant;  
 KW PRO agonist; cancer; inflammatory disorder; immunological disorder.  
 XX  
 DE Human PRO1265 protein.

Homo sapiens.

XX  
 PN WO2000073348-A2.  
 XX  
 PD 07-DEC-2000.  
 XX

PP 30-MAY-2000; 2000WO-US014941.  
 XX

PR 02-JUN-1999; 99WO-US012252.  
 PR 22-JUN-1999; 99US-014065P.  
 PR 23-JUN-1999; 99US-0141037P.  
 PR 20-JUL-1999; 99US-0144758P.  
 PR 01-SEP-1999; 99WO-US020111.  
 PR 08-SEP-1999; 99US-0162506P.  
 PR 29-OCT-1999; 99US-0162506P.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 01-DEC-1999; 99WO-US028534.  
 PR 02-DEC-1999; 99WO-US028551.  
 PR 09-DEC-1999; 99US-0170261P.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 20-DEC-1999; 99WO-US030999.  
 PR 06-JAN-2000; 2000WO-US000316.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US004341.  
 PR 02-MAR-2000; 2000WO-US004342.  
 PR 03-MAR-2000; 2000US-0187203P.  
 PR 10-MAR-2000; 2000WO-US00356.  
 PR 15-MAR-2000; 2000WO-US006894.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 17-MAY-2000; 2000WO-US013705.

(GETH ) GENENTECH INC.

Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;

Shelton DL, Smith V, Watcabe CK, Wood WI;

DR: 2001-016509/02.

N-PSDB, AAC91564.

XX  
 PT Twenty eight nucleic acids encoding PRO-polypeptides which are useful for  
 PT treating various tumors, e.g. breast cancer, and other inflammatory  
 PT angiogenic and immunological disorders.  
 XX  
 PS Claim 31; Fig 24; 189pp; English.

XX  
 CC The present sequence is one of twenty eight novel PRO polypeptides. The  
 CC PRO polypeptides and their agonists, including antibodies, peptides, and  
 CC small molecule agonists, may be used to treat various tumours, e.g.,  
 CC cancers such as breast cancer, ovarian cancer, renal cancer, colorectal  
 CC cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,  
 CC central nervous system cancer, melanoma or leukaemia. They are also  
 CC useful for treating other disorders such as neuronal, glial, astrocytal,  
 CC hypothalamic and other glandular, macrophagal, epithelial, stromal and  
 CC blastocoelic disorders, and inflammatory, angiogenic and immunological  
 CC disorders.  
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Query Match 37.0%; Score 999; ^ DB 4; Length 567;  
 Best Local Similarity 41.8%; Pred. No. 1 8e-70;  
 Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;  
 Qy 3 LHVVKWKLSVSVLITYSYHT-VALSLSKERIADCLUEDKDYDTLQLTDNGLPHINTSHH 61  
 Db 6 LHL---LVLPIPLSIVASODWKAERSQDFEKNCQDPDYEQLKVVTVGNRNLKPKR 61  
 Qy 62 VVIVGAGMAGLTAAKLLQDAGHTVTLLEANDRVRGVETVYNEKEGYAENGAMRIESSH 121  
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 Qy 242 ALSEMIDYQADVNDSTVTHVNTGSDLIPPEFLSVDVPLLNSKVKHIROSDKGTVVSY 301  
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 Qy 302 OTGNE-SLMDLSADIVLVTTAKAALFIDIDPPLSISKMEALRSVHYDSTSSTKILITFRD 360  
 Db 302 ETSPPARNLKYLUADVLUTASPVKRITPSPPPLPRMOPALRIRHYPATKVFISFR 361  
 Qy 361 KFWEDDGIRGKKSITDGPSSRYPPSHSFHTNETIGVLLASYTWSDBSLLFGASDBELK 420  
 Db 362 PFWREHIEGHSHNTDPRSMIFYPP---PREGAILLASYTWSDRAAAAPGLSREEA 416  
 Qy 421 BLALRDIAKIHG--EQVWDIKCTGVIVKVKVSDPPLSGAFAFLFTPQYQHLEYAQELLSSE- 476  
 Db 417 RLALDDVIAALHGPVVRQLWDG-TGV-VKRMADQISQGGFVYVQPP-----ALWQTEK 466  
 Qy 477 -----GRVFAGHTAFAHWIETSMSKSAIATANTN 508  
 Db 467 DDWTVPYGRYFAGGERTAYPHGMVETAVSKSALARAIKIN 505

RESULT 1.1

AAU12409  
 ID AAU12409 standard; protein; 567 AA.  
 XX  
 AC AAU12409;  
 XX  
 DT 24-OCT-2001 (first entry)  
 DE Human PRO1265 polypeptide sequence.  
 XX  
 KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;  
 KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;

ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy.

polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate Glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.

SQ	Sequence 567 AA;
Query Match	37.0%; Score 999; DB 4; Length 567;
Best Local Similarity	41.8%; Pred. No. 1-8e-70;
Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9	
Qy	3 LHYVKWKLSSVSVLTLTYSTH-VALSKEHLADCLDEDYDFTLQLTDNLGLPHNTSHH 61
Db	6 LHL---LVLPVLSSVLSAQDWKAERSDDPFEKMDDEQELLKVVTVGLNRNLTKPQR 61
Qy	62 WVIYGAGMAGLTAAKKLQDAGHTVTILEANDRVRGGRVETYRNKEGWYALMGAMPIPPSH 121
Db	62 RIVQWFGAGVAGLVAAKVLSAAGHKVTLLEADNRCGRIFTYRDONTGWLGAQMMPSSH 121
Qy	122 RIVQWFGVKKLGVENNEFWTDDNTFLYNGREPTYYVWBNPDVLYKNVSESEKEKISADD 181
Db	122 RILHKLCQGLGLNLTKFOTYDQNTWTEYHEVKLRNNVVEKVPKGKYLARPQEKGHSPE 181
Qy	182 LLDRALQKVKWEEVANGCKKALEYKDRYSVKEYLKEEGGLSPGAVRMICDNLNEQSLSMLYT 241
Db	182 IYONALNQALKDQKLRGERKAMKPERITLLEYLGEGLGENLRSRAPVQLCDMSSEGFFYI 241
Qy	242 ALSEMIIYQADVNDSVTYTHEVTCGSDLPLPEAFSLVDPLILNSKVXKH1RQSDKGIVSY 301
Db	242 SFAEALRAHSCLSDRLQPSRIVCGWDLPLRALSSLSSGLVLLNAPVVAATQGPHDVHVQI 301
Qy	302 QTGNES-SLMDLSRADIVVTTAKALFIDFDPLSISRKMEALRSVHDTSSTKLITFRD 360
Db	302 ETSPPARNLKVULKADVVLITASGPRAKRITESPLPRANQEALRRLHYPATKVLFSRR 361
Qy	361 KFWEDGIRGGKSTTGDPSRYTYP SHSFHTNETIVGILLASYTWSDESLLFLGASDEELK 420
Db	362 PFWREHTEGGHSNTDRPSRMIFP-----PPREGALLIASYTWSDAAAFAGLSREEA 416
Qy	421 ELLRLDLAKING---EQWIDKCTGIVIVKWSADPSISLGAFALFTPYQHLEYAQFLFSSE- 476
Db	417 RLALDVAALHGPPVROLWDG-TGV-VICKWAEDQHSQGFVVQGP-----ALWQTEK 466
Qy	477 -----GRVHFAGEHTAHPHAEITMSKSAIRATIN 508
Db	467 DDWTVPYGRIFAGEHTAYPHGWVETAYKSALRAIKIN 505
RESULT 1.2	
ID	ABE84904 standard; protein: 567 AA.
XX	ABE84904;
AC	
XX	(first entry)
DT	16-MAY-2002
XX	
DE	Human PRO1265 protein sequence SEQ ID NO:176.
XX	
KW	vulnerary antarteriosclerotic; PRO agonist; PRO antagonist; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; gene-related macular degeneration; arterial restraints; anoxia;
KW	angiogenesis; cardiotonic; cytoskeletal; antiangiogenic; hypotensive; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; gene-related macular degeneration; arterial restraints; anoxia;

KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
 KW wound healing; chromosome mapping; gene mapping.

Homo sapiens.

WO200200690-A2.

XX 03-JAN-2002.

PD XX 20-JUN-2001; 2001WO-US019692.

PP XX 23-JUN-2000; 2000US-0213637P.

PR PR 20-JUL-2000; 2000US-0219556P.

PR 25-JUL-2000; 2000US-0220624P.

PR PR 28-JUL-2000; 2000US-0220664P.

PR PR 02-AUG-2000; 2000WO-US020710.

PR PR 17-AUG-2000; 2000US-0226859P.

PR PR 23-AUG-2000; 2000WO-US023122.

PR PR 24-AUG-2000; 2000WO-US023128.

PR PR 07-SEP-2000; 2000US-0230978P.

PR PR 18-SEP-2000; 2000US-00664610.

PR PR 18-SEP-2000; 2000US-0065350.

PR PR 24-OCT-2000; 2000US-00643657.

PR PR 08-NOV-2000; 2000WO-US023122.

PR PR 08-NOV-2000; 2000WO-US030952.

PR PR 10-NOV-2000; 2000WO-US030973.

PR PR 01-DEC-2000; 2000WO-US032678.

PR PR 20-DEC-2000; 2000US-00747259.

PR PR 22-JAN-2001; 2000WO-US034556.

PR PR 28-FEB-2001; 2001US-00767609.

PR PR 28-FEB-2001; 2001WO-US06520.

PR PR 01-MAR-2001; 2001WO-US005666.

PR PR 09-MAR-2001; 2001US-0080276.

PR PR 14-MAR-2001; 2001US-00808689.

PR PR 22-MAR-2001; 2001US-00816744.

PR PR 05-APR-2001; 2001US-00828366.

PR PR 10-MAY-2001; 2001US-00854208.

PR PR 25-MAY-2001; 2001US-00854280.

PR PR 25-MAY-2001; 2001US-0086608.

PR PR 25-MAY-2001; 2001US-00866034.

PR PR 30-MAY-2001; 2001WO-US017092.

PR PR 30-MAY-2001; 2001US-00870574.

PR PR 01-JUN-2001; 2001WO-US017800.

XX XX (GETH ) GENENTECH INC.

PA PA Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;

PI PI Godowski PJ, Gurney AL, Hillian KJ, Marsters SA, Pan J, Paoni NF;

PI PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

XX DR DR 2002-090516/12.

DR DR N-PSDB; ABL88159.

XX XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,

PT PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial

PT PT infarction), endothelial or angiogenic disorders in a mammal.

PS PS Claim 11: Fig 176; 565pp; English.

XX XX

PA PA

PI PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;

PI PI Godowski PJ, Gurney AL, Hillian KJ, Marsters SA, Pan J, Paoni NF;

PI PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

XX DR DR 2002-090516/12.

DR DR N-PSDB; ABL88159.

XX XX

PA PA

PI PI

PI PI

PI PI

XX XX

PA PA

PI PI

PI PI

XX	25-AUG-2000; 2000US-0227818P.	Qy	421 ELALRDLAKING---EQWMDKCTGIVVKKNSADPSLGAFALFTPQHLEYAQELSSSE-
PR	XX (NSHO-) NORTH SHORE - LONG ISLAND JEWISH RES.	Db	417 RLALDVAALHPVVRQWLWDG-TGV-VKRWAEDQHQQGFVVQPP-----ALNOTEK 466
XX	Chu CC, Chavan SS, Mason JM;	Qy	477 ----GRVHPAGEHTAFAHWIETSMKSAIRAANIN 508
PI	XX	Db	467 DDWTPVIGRIYPAGEHTAPHSWETAVKSALRAAKIN 505
PT	WPI: 2002-329772/36.		
XX	New human immediate early interleukin-four (IL-4) induced protein and polynucleotides, useful for preventing or treating immune related disease, tumor, fungal or bacterial infection, e.g. lupus erythematosus or Whipple's disease.		
PS	Claim 1(a): Page 5: 61pp; English.		
XX	The invention relates to an isolated polynucleotide, which encodes a human immediate early interleukin-four (IL-4) induced protein. The activity of the polynucleotide of the invention may be described as cytostatic, antifungal, antibacterial, immunomodulator, antiinflammatory, dermatocytotoxic and immunosuppressive. The polynucleotide or antisense oligonucleotide is useful for the manufacture of a medicament for preventing, treating or ameliorating a medical condition, particularly immune related disease, tumour, fungal infection or bacterial infection. The immediate early IL-4 induced protein is useful for the manufacture of a medicament for killing unwanted cells in a mammal. The antagonist is useful for the manufacture of a medicament for use in decreasing cell death. The polynucleotide is also useful for diagnosing a pathological condition, particularly an immune related disease. These diseases may include systemic lupus erythematosus, inflammatory bowel disease, Guillain-Barre syndrome, Whipple's disease, atopic dermatitis, food hypersensitivity, rheumatoid arthritis, osteoarthritis, diabetes mellitus and psoriasis. The current polynucleotide of the invention may be used in gene therapy. The current sequence represents a human immediate early interleukin-four induced protein. Note: This sequence should be encoded by the DNA sequence given in the specification. SEQ ID 3 (Human immediate early interleukin-four induced protein genomic DNA from chromosome 19q13.3-19q13.4 - see ABU6822) - however, this does not appear to be the case.		
XX	Sequence 567 AA:		
Query Match Score 999; DB 5; Length 567; Best Local Similarity 41.8%; Pred. No. 1.be-2000; Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;	3 LHVVKWLSVSVLTLTYSHT-VALSLSKEHLADCLEDTDTLQLDGLPHINTSHH 61	PR 3 LHVVKWLSVSVLTLTYSHT-VALSLSKEHLADCLEDTDTLQLDGLPHINTSHH 61	
Qy	6 LHL---LVVPLVLLSVAQSDKAERSQDPFECMOPDPYEQQLKVWTGLNRTLKPQR 61	PR 18-SGP-2000; 2000US-0065350.	
Db	62 VVIVGAGMAGLTAALKLQDAGHTVTILEANDRYGRVETYRNKEGHVYAEQMGRIPS 121	PR 24-OCT-2000; 2000US-024922P.	
Qy	62 VVIVGAGMAGLTAALKLQDAGHTVTILEANDRYGRVETYRNKEGHVYAEQMGRIPS 121	PR 08-NOV-2000; 2000US-0079238.	
Db	62 VVIVGAGMAGLTAALKLQDAGHTVTILEANDRYGRVETYRNKEGHVYAEQMGRIPS 121	PR 07-SEP-2000; 2000US-023978P.	
Qy	122 RIVQWFVKKLVGVNNNEPFTMDDNFTYLNGVRETYVYQENPDVLYKVNSESEKGISADD 181	PR 18-SEP-2000; 2000US-0065350.	
Db	122 RILHKLKGIGLNLTKTQDKNWTEVREKGKLVNVVKEPLGYALRPQEKGHSPE 181	PR 24-OCT-2000; 2000US-024922P.	
Qy	182 LLDRALQKVEBEVANGCKALEKYDRSYKEYLKEEGGLSPGAVRMTGDLNNEQSLMYT 241	PR 08-NOV-2000; 2000US-0079238.	
Db	182 IYQMLNQALKDLKAIGCRAMKXPERHTLLEYLGEGNLRSRPAVQLGDDGMSBDGFYFL 241	PR 10-NOV-2000; 2000US-0080873.	
Qy	242 ALSEMIDQAVNDSVTYHETVGGSDLPPAFLSVLDPVILLNSKVKHROSDKGTVTSY 301	PR 01-DEC-2000; 2000US-0082678.	
Db	242 SFAEALRAHSCLSDRLIQSRLVGGMDLPRALLSSLSGLVLLNAPVVMTOQPHDVHQYQI 301	PR 20-DEC-2000; 2000US-0084956.	
Qy	302 QTGNES-SLMDSLSDVNTTAKALFIDEDPPLSISMEARSVHDTSSTKLITPRD 360	PR 22-FEB-2001; 2001US-0076769.	
Db	302 ETSPPANKLKVYKADVVLITASGPARKRITESPPLPRHNOEARRLHYYPATKVFLSRR 361	PR 28-FEB-2001; 2001US-0076498.	
Qy	361 KFWEDDGCIRGGKSITDGPSPRSITYPPSHSFHTNETGIVLLASYTWSDESLFLGASDEBK 420	PR 01-MAR-2001; 2001WO-US006520.	
Db	362 PFWREEHGSNTDRPSMLFYP----PPREGALLASYTWSDAAAFAGLSREEA 416	PR 01-MAR-2001; 2001WO-US006666.	
		PR 09-MAR-2001; 2001US-0082706.	
		PR 14-MAR-2001; 2001US-0080689.	
		PR 22-MAR-2001; 2001US-0081644.	
		PR 05-APR-2001; 2001US-0082836.	
		PR 10-MAY-2001; 2001US-0085208.	
		PR 10-MAY-2001; 2001US-0085280.	
		PR 25-MAY-2001; 2001US-00866028.	
		PR 25-MAY-2001; 2001US-00866034.	
		PR 25-MAY-2001; 2001WO-US01792.	
		PR 30-MAY-2001; 2001US-00870574.	
		PR 01-JUN-2001; 2001WO-US01743.	
		PR 20-JUN-2001; 2001WO-US017800.	
		PR 20-JUN-2001; 2001WO-US019692.	
		PR (GFTH ) GENENTECH INC.	
		PR (BAKE/ ) BAKER K. P.	
		PR (FERR/ ) FERRARA N.	
		PR (GERB/ ) GERBER H.	



PT syndrome (AIDS), or cancer.  
 XX  
 PS Claim 12; Fig 476; 660pp; English.  
 XX

The invention describes an isolated nucleic acid (I) comprising, or which has 80 % sequence identity to, or the full-length coding sequence of, one of 25 nucleotide sequences, and which encodes a corresponding polypeptide selected from 275 amino acid sequences, where all sequences are given in the specification. The polypeptide encoded by (I) is used to detect PRO polypeptides, link a bioactive molecule to a cell expressing a PRO polypeptide, modulate a biological activity of a cell, stimulate the release of tumour necrosis factor (TNF)-alpha from human blood, modulate the uptake of glucose or free fatty acid by a cell, stimulate or inhibit the proliferation or differentiation of cells or gene expression, stimulate the release of proteoglycans, stimulate the release of cytokine from peripheral blood mononuclear cells, inhibit the binding of A-peptide to factor VIIa, or detect the presence of tumour in a mammal. The nucleic acid and polypeptide encoded by it, are useful for treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, acquired immunodeficiency syndrome (AIDS), cancer, or diabetic complications. The nucleic acid is useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typing. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide

SQ

Query Match	Score	DB	Length
Best Local Similarity	999;	6;	567;
Matches	41.8%;	Pred. No.	1.8e-70;
	99;	Mismatches	171;
		Gaps	9;

Sequence 567 AA:

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 3 LHHVVKWLSTVSVLTLTYSHT - VALSLSKEHLADLEEDKDYDTLQLTDNLGLPHNTSHH 61
 6 LHL---LVLPVILSVAQDWKAKERSQDPFEKLQRQDPDQEQLKVTVTGLNRLKPKR 61
 3 LHHVVKWLSTVSVLTLTYSHTLEANDRGGRVETYRNKEKGWYAEMGAMRPSSH 121
 62 VVIVGAGMAGLTAAKLLQDAGHTVTITLEANDRGGRVETYRNKEKGWYAEMGAMRPSSH 121
 62 VVIVGAGVAGLVAAKVLQDAGHVTTLEADNRIGGRIFTYRDQNTGWIGELGAMRPSSH 121
 62 RIVQWVVKUGVEMBEFVMDTDDNTTYLNGYRERYVQENPDVTKYVNSSESEKGISADD 181
 122 RILHKUCQGLNLLKFTQDKNTWTEVHEVKLRNYYVERVKEPGKLYALRQPEQKSHPED 181
 182 LLDRDQKVKEEVEANGKALEKDVYHETVGGSDLLPPEAFSLVDVPILLSKVTHROSIDKGIVTYSV 241
 182 IYQMLNQALKDLKALGCKAMKKERHTILEYLGEGNLSRPAVQLLGDMSEGFFYFL 241
 242 ALSENMYQDADVDSVTYHEVTGGSDLLPPEAFSLVDVPILLSKVTHROSIDKGIVTYSV 301
 242 SFAELRAHSCLSDRLQYSRIVGGDLLPPEAFSLVDVPILLSKVTHROSIDKGIVTYSV 301
 302 QTGNES-SLMDSLSDIVLVTTTAKALFIDFPPISSKMEALRSVHYDSSTSCKILLFRD 360
 302 ETSPPARNTKVLKADVLLTASGPVKRITFSPPPLPRHMQEALRLHYVPAVKFLSFR 361
 361 KFWEDGIGRKSTGDSRVTIYPSHSFTNETGCVLLASYTWSBSLFLGASBDELK 420
 362 PFWREHIEGGHSNTDRPSRMIFYP --- PPREGALLASYTWSAAAAGFLSREAL 416
 421 ELALRDLAKHG---EQWDKDCTGVIVKRNNSADPYSLGAFALFTPYQHLEYAQELFSSE- 476
 417 RLALDDVAALHGPVRQLWDL-TGV-VKRAWQDQSQQGFVVQP-----ALMQTEK 466
 477 -----GRVHAGHTAFAFHAWIETSMKSAIRATNNIN 508
 467 DDWTWVGYRGIYFAGHTAYPHGWVTEAVKSALRAIKIN 505
  
```

(GETH ) GENENTECH INC.

XX

Baker KP, Beresini M, Detorge L, Desnoyers L, Filvaroff E, Gao W;  
 Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
 Smith V, Stewart TA, Tumans D, Watanabe CK, Wood WI, Zhang Z;  
 DR N-PSDB, ACD24090  
 XX

New secreted and transmembrane PRO nucleic acids, for treating inflammation, organ failure, atherosclerosis, cardiac injury, acquired immunodeficiency, birth defects, premature aging, acquired immunodeficiency

GenCore version 5.1.6  
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OM protein - protein search, using sw mode!

Run on: October 4, 2005, 13:32:30 ; Search time 43 Seconds  
(without alignments)  
909,677 Million cell updates/sec

Title: US-10-645-094-1  
Perfect score: 2703  
Sequence: 1 MNLHVVKWKLSVVSLITY.....TNINKVANEESTIHKDEL 524

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing First 45 summaries

Database : Issued\_Patents\_AA:  
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2: /cgn2\_6/pctodata/1/iaa/SB\_COMB.pep:  
3: /cgn2\_6/pctodata/1/iaa/6A\_COMB.pep:  
4: /cgn2\_6/pctodata/1/iaa/6B\_COMB.pep:  
5: /cgn2\_6/pctodata/1/iaa/PCTUS\_COMB.pep:  
6: /cgn2\_6/pctodata/1/iaa/backfile1.pep:  
\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	2703	100.0	524	3	US-09-230-388-1	Sequence 1, Appli
2	2703	100.0	524	4	US-09-912-17-1	Sequence 1, Appli
3	999	37.0	567	3	US-08-813-150-4	Sequence 4, Appli
4	999	37.0	567	4	US-09-546-553-4	Sequence 4, Appli
5	979.5	36.2	566	4	US-09-482-273-173	Sequence 173, Appli
6	488.5	18.1	320	4	US-09-482-273-267	Sequence 267, Appli
7	488.5	18.1	320	4	US-09-482-273-194	Sequence 194, Appli
8	476	17.6	275	4	US-09-482-273-265	Sequence 265, Appli
9	417	15.4	617	3	US-09-163-733A-46	Sequence 46, Appli
10	417	15.4	617	3	US-09-063-733A-56	Sequence 56, Appli
11	417	15.4	617	3	US-09-063-733A-57	Sequence 57, Appli
12	417	15.4	617	3	US-09-163-733A-58	Sequence 58, Appli
13	404	14.9	617	3	US-09-214-242-2	Sequence 2, Appli
14	392	14.5	695	3	US-09-014-244-12	Sequence 12, Appli
15	387	14.3	212	4	US-09-182-273-266	Sequence 266, Appli
16	364.5	13.5	489	4	US-09-986-536-2	Sequence 2, Appli
17	307	11.4	538	4	US-09-232-99A-16952	Sequence 16952, A
18	294	10.9	545	4	US-09-949-016-11442	Sequence 11442, A
19	283	10.5	527	1	US-08-131-168A-32	Sequence 32, Appli
20	283	10.5	531	4	US-09-949-016-11443	Sequence 11443, A
21	258	9.5	733	3	US-09-073-587-3	Sequence 3, Appli
22	211.5	7.8	458	4	US-09-328-352-7549	Sequence 7549, Appli
23	197.5	7.3	554	3	US-09-352-159-38	Sequence 17, Appli
24	197.5	7.3	554	3	US-09-552-168-17	Sequence 17, Appli
25	197.5	7.3	554	4	US-09-771-058-17	Sequence 17, Appli
26	197.5	7.3	554	4	US-09-770-56A-17	Sequence 17, Appli
27	196.5	7.3	463	4	US-09-771-045B-51	Sequence 51, Appli

## ALIGNMENTS

RESULT 1		RESULT 1	
US-09-230-388-1		US-09-230-388-1	
; Sequence 1, Application US/09230388		; Sequence 1, Application US/09230388	
; Patent No. 6291644		; Patent No. 6291644	
; GENERAL INFORMATION:		; GENERAL INFORMATION:	
; APPLICANT: Iwamoto, Mitsunori; Jung, Sang-Kee		; APPLICANT: Iwamoto, Mitsunori; Jung, Sang-Kee	
; TITLE OF INVENTION: NOVEL PROTEIN, ITS GENE, REAGENTS FOR INDUCING		; TITLE OF INVENTION: NOVEL PROTEIN, ITS GENE, REAGENTS FOR INDUCING	
; FILE REFERENCE: 4703/OF214		; FILE REFERENCE: 4703/OF214	
; CURRENT APPLICATION NUMBER: US/09/230,388		; CURRENT APPLICATION NUMBER: US/09/230,388	
; CURRENT FILING DATE: 1999-01-22		; CURRENT FILING DATE: 1999-01-22	
; PRIOR APPLICATION NUMBER: PCT/JP98/02261		; PRIOR APPLICATION NUMBER: PCT/JP98/02261	
; PRIORITY FILING DATE: 1998-05-22		; PRIORITY FILING DATE: 1998-05-22	
; NUMBER OF SEQ ID NOS: 2		; NUMBER OF SEQ ID NOS: 2	
; SOFTWARE: PatentIn Ver. 2.0		; SOFTWARE: PatentIn Ver. 2.0	
; SEQ ID NO: 1		; SEQ ID NO: 1	
; LENGTH: 524		; LENGTH: 524	
; ORGANISM: Scomber japonicus		; ORGANISM: Scomber japonicus	
US-09-230-388-1		US-09-230-388-1	

Query Match		Query Match	
Best Local Similarity 100.0%		Best Local Similarity 100.0%	
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Db 1 MNLHVVKWKLSVVSLITYLYSHTVALSKPHLADCLEDKDYTDLQLTDLNGLPHINTSH 60		Db 1 MNLHVVKWKLSVVSLITYLYSHTVALSKPHLADCLEDKDYTDLQLTDLNGLPHINTSH 60	
Qy 61 HVVIVGAGMAGLTAAKLLQDAQHTTILEANDRYGRVETYRNEKEGVTAEMGMARIPSS 120		Qy 61 HVVIVGAGMAGLTAAKLLQDAQHTTILEANDRYGRVETYRNEKEGVTAEMGMARIPSS 120	
Db 61 HVVIVGAGMAGLTAAKLLQDAQHTTILEANDRYGRVETYRNEKEGVTAEMGMARIPSS 120		Db 61 HVVIVGAGMAGLTAAKLLQDAQHTTILEANDRYGRVETYRNEKEGVTAEMGMARIPSS 120	
Qy 121 HRIIVMFVKLGIVVNEFVMTDDNTFYLVNGVRERTYYVQNPDVLYKEEGGLSPGA		Qy 121 HRIIVMFVKLGIVVNEFVMTDDNTFYLVNGVRERTYYVQNPDVLYKEEGGLSPGA	
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Qy 181 DLLDRAQKVKEEVANGCKAALKEYDRYSVKEVKEEGGLSPGA		Qy 181 DLLDRAQKVKEEVANGCKAALKEYDRYSVKEVKEEGGLSPGA	
Db 181 DLLDRAQKVKEEVANGCKAALKEYDRYSVKEVKEEGGLSPGA		Db 181 DLLDRAQKVKEEVANGCKAALKEYDRYSVKEVKEEGGLSPGA	
Qy 301 YQTGESSLMDSLADIVLVTTAKALFIDDFPPLSISKMEALRVHYDSTSKILTFRD 360		Qy 301 YQTGESSLMDSLADIVLVTTAKALFIDDFPPLSISKMEALRVHYDSTSKILTFRD 360	
Db 301 YQTGESSLMDSLADIVLVTTAKALFIDDFPPLSISKMEALRVHYDSTSKILTFRD 360		Db 301 YQTGESSLMDSLADIVLVTTAKALFIDDFPPLSISKMEALRVHYDSTSKILTFRD 360	
Qy 361 KFWEDDGIRGGKKSITDGPSRYIYPSHSFHTNETIGULLASYTNSDESULFLGASDEELK 420		Qy 361 KFWEDDGIRGGKKSITDGPSRYIYPSHSFHTNETIGULLASYTNSDESULFLGASDEELK 420	

Db 361 KFWEDDGIRGGKSITDGSRYYPPSHSFHTNETIGVLLASYTWSDESLFLGASDEELK 420

Qy 421 EIALRDLAKINGEQQWMDKCTGVIVKWSADPSLGAFAFLFTPYQHLEYAELFSSGRVH 480

Db 421 EIALRDLAKINGEQQWMDKCTGVIVKWSADPSLGAFAFLFTPYQHLEYAELFSSGRVH 480

Db 481 PAGEHTAFPHAWIETSMKSAIRATNTNKVANEESTIEHTKDEL 524

Qy 481 PAGEHTAFPHAWIETSMKSAIRATNTNKVANEESTIEHTKDEL 524

RESULT 2

US-09-912-176-1

Sequence 1, Application US/09912176

Patent No. 6619739

GENERAL INFORMATION:

APPLICANT: Iwamoto, Mitsunori; Jung, Sang-Kee

TITLE OF INVENTION: NOVEL PROTEIN, ITS GENE, REAGENTS FOR INDUCING FILE REFERENCE: 4703/08214

CURRENT APPLICATION NUMBER: US/09/912,176

PRIOR FILING DATE: 2001-07-24

PRIOR APPLICATION NUMBER: US 09/230,388

PRIOR FILING DATE: 1999-01-22

PRIOR APPLICATION NUMBER: PCT/JP98/02261

PRIOR FILING DATE: 1998-05-22

NUMBER OF SEQ ID NCS: 2

SOFTWARE: PatentIn Release #1.0, Version #1.30

SEQ ID NO 1

TYPE: PPT

ORGANISM: Scomber japonicus

us-09-912-176-1

Query Match Score 100.0%; Score 2703; DB 4; Length 524;

Best Local Similarity 100.0%; Pred. No. 3.6e-239; Length 524;

Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNHHVVKRLSVSVLTTLYSHTVALSKELHADCLDKDYDTLQLTDLGLPHINTSH 60

Db 1 MNHHVVKRLSVSVLTTLYSHTVALSKELHADCLDKDYDTLQLTDLGLPHINTSH 60

Qy 61 HVIIVGAGMAGTAALKLQDAHTVTILEANDRVRGGVETYRNEKEGWYAENGAMRIPSS 120

Db 61 HVIIVGAGMAGTAALKLQDAHTVTILEANDRVRGGVETYRNEKEGWYAENGAMRIPSS 120

Qy 121 HRIYQWFKKLGYEMNEMTDDNTFYLVNGVRERTVVOENPDVLYKVNSESEKGISAD 180

Db 121 HRIYQWFKKLGYEMNEMTDDNTFYLVNGVRERTVVOENPDVLYKVNSESEKGISAD 180

Qy 181 DLDLRAOKVKEEANGCKAALEKYDYSVKEYLKEEGGLSPGAVRMIGDLINEQSLMY 240

Db 181 DLDLRAOKVKEEANGCKAALEKYDYSVKEYLKEEGGLSPGAVRMIGDLINEQSLMY 240

Qy 241 TALSEMIYDQADYNDSDVTHYETGGSDILPEAFLSVLDVPIILLNSKVYKHIOSDKGVIVS 300

Db 241 TALSEMIYDQADYNDSDVTHYETGGSDILPEAFLSVLDVPIILLNSKVYKHIOSDKGVIVS 300

Qy 301 YOTGNESSIMLSDADIYLVTTAKAALFIDFDPLLSKMEALRSYHYDSSTKILLTFRD 360

Db 301 YOTGNESSIMLSDADIYLVTTAKAALFIDFDPLLSKMEALRSYHYDSSTKILLTFRD 360

Qy 361 KFWEDDGIRGGKSITDGSRYYPPSHSFHTNETIGVLLASYTWSDESLFLGASDEELK 420

Db 361 KFWEDDGIRGGKSITDGSRYYPPSHSFHTNETIGVLLASYTWSDESLFLGASDEELK 420

Qy 421 EIALRDLAKINGEQQWMDKCTGVIVKWSADPSLGAFAFLFTPYQHLEYAELFSSGRVH 480

Db 421 EIALRDLAKINGEQQWMDKCTGVIVKWSADPSLGAFAFLFTPYQHLEYAELFSSGRVH 480

Qy 481 PAGEHTAFPHAWIETSMKSAIRATNTNKVANEESTIEHTKDEL 524

Db 481 PAGEHTAFPHAWIETSMKSAIRATNTNKVANEESTIEHTKDEL 524

RESULT 3

US-08-813-150-4

Sequence 4, Application US/08813150

GENERAL INFORMATION:

APPLICANT: Mueller, Christopher Lebecque, Serge J.E.

APPLICANT: Liu, Yong-jun Dowling, Lynette M.

APPLICANT: Huffine, Constance M.

APPLICANT: Gorman, Daniel M.

TITLE OF INVENTION: MAMMALIAN PROTEINASES ; OXIDOREDUCTASES ; RELATED REAGENTS

TITLE OF INVENTION: RELATED REAGENTS

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: DNAX Research Institute

STREET: 901 California Avenue

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/813,150

FILING DATE: 07-MAR-1997

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Chung, Edwin P.

REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: SF0693

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-552-9196

TELEFAX: 650-496-1200

INFORMATION FOR SEQ ID NO 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 567 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

us-08-813-150-4

Query Match Score 999; DB 3; Length 567;

Best Local Similarity 41.8%; Pred. No. 9.3e-83;

Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

Qy 3 LHHVWKRLSVSVLTTLYSHT-VALSLSKELHADCLDKDYDTLQLTDLGLPHINTSH 61

Db 6 LHL---LVLPVILLSVASODWKAEERSQDPFEKCMODPDEQKUVTVGLNRNLTKPQR 61

Qy 62 VVIVGAGMAGTAALKLQDAHTVTILEANDRVRGGVETYRNEKEGWYAENGAMRIPSS 121

Db 62 VVIVGAGVAGLVAAKVYLSDAHGKVTILEADNRIGGIFTYRDQNTGWIGLAMRMPSSH 121

Qy 122 RIVQWFKKLGYEMNEMFVMTDDNTFYLVNGVRERTVVOENPDVLYKVNSESEKGISADD 181

Db 122 RILHKLQCGLGILNLTQFTQDKNTEVEHEVTLRNYVVEPKQEGHSPEED 181

Qy 182 LLDRALQVKREBEVANGCKALEKYDYSVKEYLKEEGGLSPGAVRMIGDLINEQSLMYT 241

Db 182 IYQMLNQALKDALKGCRVAKMKEPERTULLEYLGEGNLNSRPAVQGLGDMSEDFFFYL 241

Qy 242 ALSEMIDYQADYNDSDVTHYETGGSDILPEAFLSVLDVPIILLNSKVYKHIOSDKGVIVS 301

Db 242 SPAELRAHSCSLRQLQYSRIVGNDLPLRALLSLSGLVLLNAPVUAMTQGPHDVHVQI 301

Qy

Qy 302 QTGNES-SLMLDLADIYVTTAKAALFDIDPLLSIKMEARSVHSDSSKTIKLTFRD 360  
Db 302 ETSPPRNLKVKLADVVILTAGSPAVKRITESPPLPRMQLEARRLHYVPAKVLSSRR 361  
Qy 361 KFWBDDGIRGGKSITDGPSRYIYPSPHSFTNINETIGVLLASYTWSDESLFLGASDEELK 420  
Db 362 PFPREEHIEGGHSITDPSRMIFP-----PPREGALLASYTWSDESLFLGASREEL 416  
Qy 421 ELALRDIAKTH---EQYNDKCTGVKWKSAADPSLGAFALFTPYQHLEYAQELFSSS- 476  
Db 417 RLALDDVAALHGPGVVRQWMDG-TGV-VKRWAEQDHSQGSFVQPP-----ALWOTEK 466  
Qy 477 -----GRVHFAGEHTAAPHAWIETSMKSAIRATNN 508  
Db 467 DDWTVPYGRIVFAGEHTAYPHGVWETAVSKSALARAIKIN 505

RESULT 4  
US-09-546-553-4  
Sequence 4, Application US/09546553  
Patent No. 6534605  
GENERAL INFORMATION:  
APPLICANT: Mueller, Christopher  
APPLICANT: Lebecque, Serge J.E.  
APPLICANT: Liu, Yong-Jun  
APPLICANT: Dowling, Lynette M.  
APPLICANT: Gorman, Constance M.  
APPLICANT: Gorman, Daniel M.  
TITLE OF INVENTION: MAMMALIAN PROTEINASES ; OXIDOREDUCTASES ;  
TITLE OF INVENTION: RELATED REAGENTS  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNA Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94104-1104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/546,553  
FILING DATE: 10-APR-2000  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/813,150  
FILING DATE: 07-MAR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.  
REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: SP0693  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-852-9196  
TELEFAX: 650-496-1200  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 567 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-546-553-4

Query Match Score: 999; DB 4; Length: 567;  
Best Local Similarity 41.8%; Pred. No. 9; 3e-83;  
Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;  
3 LHVVKKWLSSVSVLITLYYYSH-VALSLLKEHLADCLEDKDYYDTLQLTDNGLPHINTSHH 61  
6 LHL-----LVLPILLSLVASQDKWAERSQDFEKCMQDPDFEQLLKVTWGLNRTLKPQR 61  
Qy 62 VVVGAGMAGLTAAKLLDQDGHFTVILEANDRGGRVETYRNKEKGWYAENGAMRIPSSH 121  
Db 62 VVVGAGVAGLVAARYLSDAGHKVTLIENDRIGGFTDQNTGWIGELGAMRMPSSH 121  
Qy 122 RIVONFVKLGVEMNEFVMDDNTFYLNVGGRERTTYQENPDVLKYVNSESEKGISADD 181  
Db 122 RILHKLQCGQGLSNLNTKFQDQNTWVEKVEBKLGALPQERGHSPBD 181  
Qy 182 LLDRALQKVKEVEANGCKAALEKDYRSKEYLKEBGGLSRGAVNMIGDLNNEQSLMYT 241  
Db 182 IYOMALNQALKDLKALGCRKAMKKFERHTLEYLGGNLNSRPAVQQLGDVNSEDGFSYL 241  
Qy 242 ALSEMIDQADVNDSVYTHEVGGSDLIPEFLSFLDVPILLNSKVKHIRDSDKGTVVSY 301  
Db 242 SPAEALRAHSCSLDRQYSRIVGGDWLPLRALLSSLGLVLLNAPVAMTQGPHDVHQVJ 301  
Qy 302 QTGNESS-LMDSLSDAIVLVTTAKAALFIDFDPLLSKMEALRSVHYDSSSTKILLTFRD 360  
Db 302 ETSPPARNLKVLKADVVLTAGSPAVRITSPPLPRHMQEALRRLHVTPAKVFLASR 361  
Qy 361 KFWEDDGIRGGKSITDGPSRYIYPSPHSFTNINETIGVLLASYTWSDESLFLGASDEELK 420  
Db 362 PFWREBHEIEGHSHNTDRPSRMIFP----PPREGALLASYTWSDEAAAFAGLSREBAL 416  
Qy 421 ELALRDIAKTH---EQYWDICGTGVTKWNSADPSYSGAFALFTPYQHLEYAQELFSSS- 476  
Db 417 RLALDDVAALHGPGVVRQWMDG-TGV-VKRWAEQDHSQGSFVQPP-----ALWOTEK 466  
Qy 477 -----GRVHFAGEHTAAPHAWIETSMKSAIRATNN 508  
Db 467 DDWTVPYGRIVFAGEHTAYPHGVWETAVSKSALARAIKIN 505

RESULT 5  
US-09-482-273-173  
Sequence 173, Application US/09482273  
Patent No. 6534631  
GENERAL INFORMATION:  
APPLICANT: Roben et al.  
TITLE OF INVENTION: 71 Human Secreted Proteins  
FILE REFERENCE: P2030P1  
CURRENT APPLICATION NUMBER: US/09/482,273  
CURRENT FILING DATE: 2000-01-13  
EARLIER APPLICATION NUMBER: PCT/US99/15849  
EARLIER FILING DATE: 1999-07-14  
EARLIER APPLICATION NUMBER: 60-092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60-092,922  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60-092,956  
EARLIER FILING DATE: 1998-07-15  
NUMBER OF SEQ ID NOS: 267  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 173  
LENGTH: 566  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-482-273-173

Query Match Score: 979.3; DB 4; Length: 566;  
Best Local Similarity 41.4%; Pred. No. 5.7e-81;  
Matches 215; Conservative 99; Mismatches 172; Indels 33; Gaps 10;

Qy 3 LHVVKKWLSSVSVLITLYYYSH-VALSLLKEHLADCLEDKDYYDTLQLTDNGLPHINTSHH 61  
Db 6 LHL-----LVLPILLSLVASQDKWAERSQDFEKCMQDPDFEQLLKVTWGLNRTLKPQR 61  
Qy 62 VVVGAGMAGLTAAKLLDQDGHFTVILEANDRGGRVETYRNKEKGWYAENGAMRIPSSH 121  
Db 62 VVVGAGVAGLVAARYLSDAGHKVTLIENDRIGGFTDQNTGWIGELGAMRMPSSH 121  
Qy 122 RIVONFVKLGVEMNEFVMDDNTFYLNVGGRERTTYQENPDVLKYVNSESEKGISADD 181

62 VVIVGAGNAGLTAALKLQDAHTVTILEANDRVGRVETYRNKEGYAEMGAMRIPSSH 121  
 48 -----  
 Db 122 RILHKLCQGLGNLTKEFYDKNTWTEVEVKLRRNYYVEKVKPEKUGYALRPQEKGHSPPD 181  
 Qy 182 LIDRALQKVEEANGCKAALEKYDYSKEYLKKEBGGSPGAVRMIGJULLNEOSLMYT 241  
 Db 182 IYOMALNQALDKLAKGCKRKMKFERTTLEYLGEGNLNSPAVQLLGDSMSEDFFFYL 241  
 Qy 242 ALSEMITYQADYNDSTYTHEVTCGSIDLPEAFSLVDPTILLNSKVTKHTRSDKCVTYSY 301  
 Db 242 SFAEALRAHSCLSDRLQYSRITVGWDLPLRALLISSLGLVILNAPVAMTQGPDVHVI 301  
 Qy 302 QTGNES-SLMDSLADIUVTTAKAALFIDPDPPLSISKMEALRSVSYHDSSTKILLTFRD 360  
 Db 302 ETSPPARNLKVKLADVULLTASGPVFRITESPPLPRHMOCALRHYHPATKVLSSFR 361  
 Qy 361 KWEEDDDGTRGGSIITDGPSRYIVYPSHFSHNETIGVLASYTAWDESLFLIGASDEELK 420  
 Db 362 PFWREEHIEEGHSNTDRPSRMIFYP---PEREGALLASYTWSDAAAAPAGLSREAL 416  
 Qy 421 ELALRDLIAKIHG--EQWWDKCTGVITKRWADPYSIGAFAFLTPYQHLEYAQELESSE- 476  
 Db 417 RLADDVVALHGTVQWWDG-TGV-WKRWADQHSGCFTVQWP-----ALWOTEK 466  
 RESULT 7  
 US-09-482-273-194  
 ; Sequence 194, Application US/094822273  
 ; Patent No. 6534631  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: 71. Human Secreted Proteins  
 ; FILE REFERENCE: PZ030P1  
 ; CURRENT APPLICATION NUMBER: US/09/482,273  
 ; EARLIER APPLICATION NUMBER: PCT/US99/15849  
 ; EARLIER FILING DATE: 1999-07-14  
 ; EARLIER APPLICATION NUMBER: 60/092,921  
 ; EARLIER FILING DATE: 1998-07-15  
 ; EARLIER APPLICATION NUMBER: 60/092,922  
 ; EARLIER FILING DATE: 1998-07-15  
 ; EARLIER APPLICATION NUMBER: 60/092,956  
 ; EARLIER FILING DATE: 1998-07-15  
 ; NUMBER OF SEQ ID NOS: 267  
 ; SEQ ID NO 194  
 ; TYPE: PRT  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; LENGTH: 320  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 ; ORGANISM: Homo sapiens  
 ; FEATURE: SITE  
 ; NAME/KEY: SITE  
 ; LOCATION: (115)  
 ; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids  
 ; FEATURE: SITE  
 ; NAME/KEY: SITE  
 ; LOCATION: (320)  
 ; OTHER INFORMATION: Xaa equals stop translation  
 US-09-482-273-194  
 Query Match 18.1%; Score 488.5; DB 4; Length 320;  
 Best Local Similarity 33.6%; Pred. No. 2.6e-36;  
 Matches 112; Conservative 69; Mismatches 109; Indels 43; Gaps 4;  
 Qy 3 LHVVWKWLSSVSVLITYLTYSH-TVALSLSKHLADCLUEDKDYLQTLQTDNGLPHINTSHH 61  
 Db 6 LHLL---LVLYVPIISSLVVASQDWKAERSQDPFEKCMQDPYEQLK-----47  
 Qy 62 VVIVGAGNAGLTAALKLQDAHTVTILEANDRVGRVETYRNKEGYAEMGAMRIPSSH 121  
 Db -----

48 -----VTLBADNRIGGRIFTYRDXTGWIGELGAMRMPSSH 84  
 Db 122 RIVQWFVKLGVENNEFMTDDNTFYLYNGVRRTYVQENPDVLYKVNVSSEBKGISADD 181  
 Qy 85 RILHKLCQGLNLTKFVQDNTWTEHXKLRYVTEKVPEKGLYALRPDKGHSIDP 144  
 Db 182 LLDRALQVKVEEYANGCKAALKEKYDRSYKEYLKEERGGLSPGAVMGDLJLNEQSLMYT 241  
 Qy 145 IVOMALNAGALKDULKALEGKMKFPERLTLEYLLGENLSRPAVQLGDMSEDGFYI 204  
 Db 242 ALSEMIYQADYNDSDVTYTHEVTCGSDLILPEAFISVLVDILLNSKVKHRSQDKGYTVSY 301  
 Qy 205 SPAEALRAXSCLSDRLQYSLRIVGWDULPRALISSLSCLVLLNAPVYMTQPHDVHQVI 264  
 Qy 302 QTGNES-SLMDSADIVAVTPTAKAALFTDFDP 333  
 Db 265 ETSPPARNVLKVLKADVVLITASGPVKRITFSP 297

**RESULT 8**  
 US-09-482-273-265  
 Patent No. 6534631  
 GENERAL INFORMATION:  
 APPLICANT: Rosen et al.  
 TITLE OF INVENTION: Human Secreted Proteins  
 FILE REFERENCE: P2030P1  
 CURRENT APPLICATION NUMBER: US/09/482,273  
 CURRENT FILING DATE: 2000-01-13  
 EARLIER APPLICATION NUMBER: PCT/US99/15849  
 EARLIER FILING DATE: 1999-07-14  
 EARLIER APPLICATION NUMBER: 60/092,921  
 EARLIER FILING DATE: 1998-07-15  
 EARLIER APPLICATION NUMBER: 60/092,922  
 EARLIER FILING DATE: 1998-07-15  
 EARLIER APPLICATION NUMBER: 60/092,956  
 EARLIER FILING DATE: 1998-07-15  
 NUMBER OF SEQ ID NOS: 267  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 265  
 LENGTH: 275  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE: NAME/KEY: SITE  
 LOCATION: (47)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 FEATURE: NAME/KEY: SITE  
 LOCATION: (94)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 FEATURE: NAME/KEY: SITE  
 LOCATION: (192)  
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 us-09-482-273-265

Query Match 17.6%; Score 476; DB 4; Length 275;  
 Best Local Similarity 34.7%; Pred. No. 2.8e-35;  
 Matches 103; Conservative 62; Mismatches 94; Indels 38; Gaps 2;

36 CLEDKDYDTLQLTDNLPHINTSHHVVIVGAGMAGLTAALKLQDAGHTVTRILEANDRVG 95  
 :|||:|||:|||:  
 15 CMQDPDYEOLRK-----VTELEADRNRIG 37

Db 168 YNVSESEKGISADDLDRALQKV-----KEEVBANGCKA-ALEKYDRYSVKSYLKKE 218  
 Qy 96 GRVETNRNEKEWYAENGAMRIPSSHRIIVQWFVKLGVMNFVMDNTFYLYNGVRBR 155  
 Db 193 YMVSTANGTVPDDVDSVGEKLOQAFGYKEKLAEFDQGFDDELMLVDMDMTTREYLKRG 252  
 Db 38 GRIFTYRDQXGTWIGELGAMMMPSSHRLHKLCQGLLNLTKPTQDKNTWTEHEXLKR 97

Qy 156 TVVQENPDVLYKVNVSSEBKGISADDLDRALQKVKEEYANGCKAALKEKYDRSYKEYL 215  
 Db 219 G-GISPG----AVRMIGDLINEQSMLMYTASEMMYDQADYNDSV--TYHEVTGSDLLP 270  
 Qy 253 GPKGEPKYDFAIQMTEMOTQNTGTMFLDQAFSESTIDSFDNPXPMEWICEGGTSSLV 312  
 Db 271 EAFLSVLDVPTLNSKVKHIR---QSDKGKVIVSQTGNESSSLMDLSADIWLVTTTAKAA 326

Qy 216 KREGGLSPGAVRMIGDLINEQSMLMYTASEMMYDQADYNDSVTYHEVTGSDLLPBEAFLS 275  
 Db 158 LGEUNISRPAVQGDMSEDFFYUFSFABALRAXSCLSDRLPRAALS 217  
 Qy 276 VLDVPLLNSKVKHRSQDKGYTVISYOTGNES-SLMDSADIVLVTTTAKAALFDF 331  
 Db 218 SLSGGLVLLNAPVYMTQGPHDVHQIETSPPARNLKVLKADVVLITASGPVKRITF 274

RESULT 9  
 US-09-063-733A-46  
 / Sequence 46, Application US/09063733A  
 / Patent No. 6372211  
 / GENERAL INFORMATION:  
 / APPLICANT: Greenplate, John T.  
 / APPLICANT: Purcell, John P.  
 / APPLICANT: Romano, Charles P.  
 / TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING  
 / TITLE OF INVENTION: INSECTS  
 / NUMBER OF SEQUENCES: 58  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: Arnold White & Durkee  
 / STREET: PO Box 4433  
 / CITY: Houston  
 / STATE: TX USA  
 / ZIP: 77210-4433  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Floppy disk  
 / COMPUTER: IBM PC Compatible  
 / OPERATING SYSTEM: PC-DOS/Ms-DOS  
 / SOFTWARE: PatentIn Release #1.0, Version #1.30  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/09/063, 733A  
 / FILING DATE: 21-APR-1998  
 / CLASSIFICATION: 435  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: Patterson, Melinda L.  
 / REGISTRATION NUMBER: 33,062  
 / REFERENCE/DOCKET NUMBER: MOBT:022  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: 713-787-1400  
 / TELEFAX: 713-787-1440  
 / INFORMATION FOR SEQ ID NO: 46:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 617 amino acids  
 / TYPE: amino acid  
 / STRANDEDNESS: not relevant  
 / TOPOLOGY: Linear  
 us-09-063-733A-46

Query Match 15.4%; Score 417; DB 3; Length 617;  
 Best Local Similarity 31.0%; Pred. No. 2.7e-29;  
 Matches 156; Conservative 83; Mismatches 177; Indels 88; Gaps 26;

Qy 62 VVIVGAGMAGLTAALKLQD--AGHTVTRILBANDRVGGRVET--YRNKEKGWYAENGAMR 116  
 Db 87 VCIVGAGVGSGLYIAMLDLKIPLNITYDIFESSSRGGRYLYTHHFTDAKHDYY-DGMAR 145  
 Qy 117 ---IPPSHRIVQWFVKLGVMNEFVMTDDNTFYLVN-----GYRERTYVQENPDVLK 167  
 Qy 62 VVIVGAGMAGLTAALKLQD--AGHTVTRILBANDRVGGRVET--YRNKEKGWYAENGAMR 116  
 Db 87 VCIVGAGVGSGLYIAMLDLKIPLNITYDIFESSSRGGRYLYTHHFTDAKHDYY-DGMAR 145  
 Qy 146 YPDIPMCKRTENLFKRTGHPLIKYLQDGTENPQLYNNHFAKGYSDF-----P 192

Qy 168 YNVSESEKGISADDLDRALQKV-----KEEVBANGCKA-ALEKYDRYSVKSYLKKE 218  
 Db 193 YMVSTANGTVPDDVDSVGEKLOQAFGYKEKLAEFDQGFDDELMLVDMDMTTREYLKRG 252

Qy 219 G-GISPG----AVRMIGDLINEQSMLMYTASEMMYDQADYNDSV--TYHEVTGSDLLP 270

Qy 253 GPKGEPKYDFAIQMTEMOTQNTGTMFLDQAFSESTIDSFDNPXPMEWICEGGTSSLV 312

Qy 271 EAFLSVLDVPTLNSKVKHIR---QSDKGKVIVSQTGNESSSLMDLSADIWLVTTTAKAA 326



Query Match Similarity 15.4%; Score 417; DB 3; Length 617;  
 Best Local Similarity 31.0%; Pred. No. 2.re-29;

Matches 156; Conservative 83; Mismatches 177; Indels 88; Gaps 26;

Qy 62 VVIVGAGAGLITAALKLQD--AGHTVITLEANDRVRGGRVET--YRNKEGHYAAEMGAMR 116  
 Db 87 VCIVGAGSGLYATMILDDKLKIPNLTYDIFESSRTGCRLYTHFTDAKHDDY-DIGAMR 145

Qy 117 ---IPSSRIVQVFVKKGIVKENEFVMTDDNTFLVN---GVRETRYVQENPVLK 167  
 Db 146 YPDIPSMKRTPNLF-KRTGMLPLIKYUULLGENTPQLYNHFFAKGVSD---P 192

Qy 168 YNVESEKGISADDLDRALQKV-----KEEVEANGCKA-ALEKYDRYSVKEYLKEE 218  
 Db 193 YMVSANGSTVQDVEGLQQARFYKEXKLAEDFDKGFDDELMLVDDMTTREYLKRG 252

Qy 219 G--GLSPG---AVRMIDDLNBQSLMVTALSEMIVYQADVNDSV--TYHEVTGGSDLLP 270  
 Db 253 GPKGEAPKDYDFPAIQMNETQNTGTNLFPQAFSESVIDSFDNFNPTKPEWYCIEGGTSLLV 312

Qy 271 EAFLSVLVPILLNSKWHIR---OSKGIVIVSYQTCNESSLMIDSADIVLVTTAKAA 326  
 Db 313 DAMKETLTHVQNKRVDIASTDLDAPPDG-NMSVR.GK---DHSGYSTVENTALGC 367

Qy 327 L-----FIDFDPLSISKMEALRSVHYDSSTKILLFRDKFW-EDDGIR GGKSITDGP 378  
 Db 368 LDMDLRLQRNLNP----TQADALRCHYDNSTKVALKFSYPMWIKOCGITECGGAASSTDLP 423

Qy 379 SRVYYPPHSF-HTNETIGVLLASYTWSDESLIFLGA-----SDEELKEELALRDL 427  
 Db 424 LRTCVYESYNLDDTG-E-AVLLASYTWSQDATR-IGSLVKAOPQPDKEDELVELLQLN 480

Qy 428 AKIHG----EQWDKCTGVI-VKKWNPDRDPSLGAFAFTPYQHLEYAQELF--SSEGKV 479  
 Db 481 ARIHAENITYKEIKEYATGVHAYCWANDPNVGGAFALFGPQFSNLYPYLMRPAAGKF 540

Qy 480 HPGAEHTAPPHAWIETSMKAIRA 503  
 Db 541 HVGEASSHHAWIIGSLESAYTA 564

RESULT 12  
 US-09-063-713A-59  
 ; Sequence 58, Application US/09063733A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Isaac, Barbara G.  
 ; APPLICANT: Greenplate, John T.  
 ; APPLICANT: Purcell, John P.  
 ; APPLICANT: Romano, Charles P.  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING  
 ; NUMBER OF SEQUENCES: 58  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Arnold White & Durkee  
 ; STREET: PO Box 4433  
 ; CITY: Houston  
 ; STATE: TX  
 ; COUNTRY: USA  
 ; ZIP: 77210-4433  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/063,733A  
 ; FILING DATE: 21-APR-1998  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Patterson, Melinda L.  
 ; REGISTRATION NUMBER: 33,062

RESULT 13  
 US-09-314-242-2  
 ; Sequence 2, Application US/09314242A  
 ; Patent No. 6248575  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Elizabeth J. Golightly  
 ; TITLE OF INVENTION: Nucleic Acids Encoding Polypeptides  
 ; FILE REFERENCE: 5556.20-US  
 ; CURRENT APPLICATION NUMBER: US/09/314,242A  
 ; CURRENT FILING DATE: 1999-05-18  
 ; EARLIER APPLICATION NUMBER: 09/080,428  
 ; EARLIER FILING DATE: 1998-05-18  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO: 2  
 ; LENGTH: 617  
 ; TYPE: PRT  
 ; ORGANISM: Trichoderma harzianum  
 ; US-09-314-242-2

Query Match Score 404; DB 3; Length 617;  
 Best Local Similarity 30.6%; Pred. No. 4.2e-28;  
 Matches 154; Conservative 84; Mismatches 178; Indels 88; Gaps 26;

Qy 62 VVIVGAGAGIQTAAKUQLQD--AGHTWTTILEBANDRVRGRT--YRNKEKGWYAEMGAMR 116  
 Db 87 VCVAGAGVSGLYTAMIIDDLKLPNLTYDIFESSSRTRGRLYTHHFTDAKHYY-DIGAMR 145

Qy 117 --IPSSHRIQWPKVKKLGVMNEFVNDDNTFYLNVGVRERTYVQENPDV-LCKNVSSEKGISADDLL 167  
 Db 146 YDPDSMKRTEFLNFK-TKTMPLIKYLDGENTPOLYNNHFFAKGVSD--P 192

Qy 168 YNVESESEGIGSADDLLRALARQV-----KEVEANGCRA-ALEKYDRYSKEYLKEE 218  
 Db 193 YMVSVANGGTVPDDVVDSVGEKLQQAFGGYYKEKLAEDFKGFDLMDMTREYLKRG 252

Qy 219 G--GLSPG---AVRMIGDLINBOSLMTAISEMIMYQADVNDSV-TYHEVTGGSDLILP 270  
 Db 253 GPKGEADPKYDFFAIQNMETQNTGTNLFDQAFSESEVIDSFEDNPPTKPEWICIEGGTSLLV 312

Qy 271 EAFLSVLDVPIILNSKVKHIR---QSDKGTVIVSYQTGNESSLMLSDAIDIWLVTTAKAA 326  
 Db 313 DAMEKTLVHKVQNNKRDAISIDDAFDG-NMSVRIGK---EHISGYSTVENTALGC 367

Qy 327 L-----FIDFPDPLSTSMEALRSYDSTSSTKILLTFRDKFW-BDDGIR-GGKSITDGP 378  
 Db 368 LDRMDLRGLGNLHP---TQADAIRCLHYDNSTKVALKFSYPMWIKDCGTTGGAESTDLP 423

Qy 379 SRYIYYPSHSF-HTNETTIVGULLASYTWSDESILFLGA-----SDEELKELALRDL 427  
 Db 424 LRTCVPYPSYNLADTG--AVLLASYTWSQDATR-IGSLVKBAPPQPKEDLVELLILQNL 480

Qy 428 AKIHG----EQYWDKCTGVIV-VKKNSADPISLGAFLFTYQHLEYAQELF--SSEGGRV 479  
 Db 481 ARLHAEHMTYEKIKEATGVYTHAYCNANDPNYGGAFALFGPCQFSNLYPYLMRPAAGKF 540

Qy 480 HPGAEHTAPPHAWIETSMKSARA 503  
 Db 541 HTVGEASSVHHAWIIGSLESAYTA 564

RESULT 14  
 US-09-314-242-12  
 ; Sequence 12, Application US/09314242A  
 ; Patent No. 6248575  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Elizabeth J. Golightly  
 ; TITLE OF INVENTION: Nucleic Acids Encoding Polypeptides  
 ; TITLE OF INVENTION: Having L-Amino Acid Oxidase Activity  
 ; FILE REFERENCE: 5546.200-US  
 ; CURRENT APPLICATION NUMBER: US/09/314,242A  
 ; CURRENT FILING DATE: 1999-05-18  
 ; EARLIER APPLICATION NUMBER: 09/080,428  
 ; EARLIER FILING DATE: 1998-05-18  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: FastaSeq for Windows Version 3.0  
 ; SEQ ID NO: 12  
 ; LENGTH: 695  
 ; TYPE: PRT  
 ; ORGANISM: Trichoderma harzianum  
 ; US-09-314-242-12

Query Match Score 392; DB 3; Length 695;  
 Best Local Similarity 27.0%; Pred. No. 6.4e-27;  
 Matches 148; Conservative 90; Mismatches 195; Indels 116; Gaps 26;

Qy 37 LEDKDYDTLQLDNGLFHINTSHHHVVGAGMAGLTAAKLUQDAGT-VTILEANDRVG 95  
 Db 160 LEDKE----ISTVD---VEKAKSKNIAVGAAGMSGMINTYLCHTOAGNTIVSIIEGGNRLG 212

Qy 96 GRVET-----YRNKEKGWYAEMGAMRIP-----SSHRIV-----PREGALLA 124  
 Db 7 EALRDRHYVPAKVFILSFRPFWRERBEHCGHSNTDRPSRMIFYP---PPREGALLA 61

213 GRVHTBYLSCGGPFDYS-----YQEMGPMRFPTNTITLGNETVNYSDHOLVFQLAEMNSL 266  
 125 QWFVFKLGVMNEFVNDDNTFYLNVGVRERTYVQENPDV-LCKNVSSEKGISADDLL 183  
 Db 267 NGHSKNLSDVEIPWVQNSNGLYYDGK-----NPETGLPPTLAE---LAANSSL 314  
 Qy 184 DRALQKVKEEANGCOKAALEKVDYR-SVKEYLKE-----EGGLSPGAVRMIGDL 232  
 Db 315 --ALTRVSN---NSTSKLSQKVDPFLPDPDKFLPEMAQNMFKAHDWISGGLAGLPDQ 368  
 Qy 233 LNEQSMTYALSEMYYQADQDMSV-----YHEVTGSDLLPEAFPLSVL 277  
 Db 369 WSEFGFMVNLYRGSUNDTAFLAPAUSTRGTRCTKGCTFPRRGAIDGGLNRPLSFHPLV 428  
 Qy 278 DVPILNLNSKVKHII--ROSPDKGVII--VSYOTGNESLMDSLADIVLVTTAKALFIDF 331  
 Db 429 DNATLNRLLERVA-DAETOKVTLISRSNYSKDSFESS---EHDAVIAAPPSTIKKWRF 484  
 Qy 332 DPPLISK--MEALRSYHDSSTSSTKILLTFRDKFWB-DDGIRGCKSIT-DGPS-RYIYV 384  
 Db 485 SPALDITAPTLANAQNLETSSACVAKERTRFBBHLPOPIYGCSRTSDIGGSIICY 544  
 Qy 385 PSHTSHTNETTIGVLLASY---TWIDESLFLPGASDEELKELALRDLAKINGEQ-VWDKC 439  
 Db 545 PSYNNNGTDPASTILASYSIGSADNGDR--WVSTTBEEHVQYLNAMAELTHEELVKEQY 601  
 Qy 440 TGVIVRK--WSADPYSLGAGAFLTPYQHLEYAQELFSSEGRVHFAGBHTAFAPHAWIETSMK 498  
 Db 602 TGQFNRCWALDPLLEASASWASPTVCOHBLVLPPEYFOTRNLVVFGEHTSYTHAWASALE 661  
 Qy 499 SAIRATNI 507  
 Db 662 SGIRSQVL 670

RESULT 15  
 US-09-482-273-266  
 ; Sequence 266, Application US/09482273  
 ; Patent No. 6534631  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: 71 Human Secreted Proteins  
 ; FILE REFERENCE: P2030P1  
 ; CURRENT APPLICATION NUMBER: US/09/482,273  
 ; CURRENT FILING DATE: 2000-01-13  
 ; EARLIER APPLICATION NUMBER: PCT/US99/15849  
 ; EARLIER FILING DATE: 1999-07-14  
 ; EARLIER APPLICATION NUMBER: 60/092,321  
 ; EARLIER FILING DATE: 1998-07-15  
 ; EARLIER APPLICATION NUMBER: 60/092,922  
 ; EARLIER FILING DATE: 1998-07-15  
 ; EARLIER APPLICATION NUMBER: 60/092,956  
 ; EARLIER FILING DATE: 1998-07-15  
 ; NUMBER OF SEQ ID NOS: 267  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 266  
 ; LENGTH: 212  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: SITE  
 ; LOCATION: (123)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 US-09-482-273-266

Query Match Score 387; DB 4; Length 212;  
 Best Local Similarity 46.9%; Pred. No. 2.7e-27;  
 Matches 84; Conservative 25; Mismatches 44; Indels 26; Gaps 6;  
 Qy 341 EALRSHYDSSSTKILLTFRDKFWEDGIRGCKSITDGPSPSYIYVYSHSFETNETIGVLLA 400  
 Db 7 EALRDRHYVPAKVFILSFRPFWRERBEHCGHSNTDRPSRMIFYP---PPREGALLA 61

Oy 401 SYTWSDESLLFUGASDEBLKELALRDLAKIHG---EQWWDKCTGIVVKKWSADPYSTGAF 457  
Db 62 SYTWSDAAAFAGLSREBALRLADDYALHGPVRQWDG-TGV-YKRWAIDQHSQGF 119

Oy 458 ALPPTPYQHLEYAOBLFSSB-----GRVHPAGEHTAPPHAMIEITSMSKAIRAAATMIN 508  
Db 120 VVQXP-----ALWQTEKDMDTVPYCRIVPAGEHTAPPHCWETAVKSALRAA1KIN 170

Search completed: October 4, 2005, 13:48:06  
Job time : 45 secs

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			Result No.	Score	Query Match Length DB ID	Description
OM protein - protein search, using sw model			1	2703	100.0	Sequence 1, Appli
Run on:	October 4, 2005, 13:40:50 ; Search time 479 Seconds (without alignments)		2	2703	100.0	Sequence 1, Appli
	1277.735 Million cell updates/sec		3	2703	100.0	Sequence 1, Appli
			4	1063.5	39.3	Sequence 143961,
Title:	US-10-645-094-1		5	1059.5	39.2	Sequence 131193,
Perfect Score:	2703		6	1034	38.3	Sequence 143903,
Sequence:	1 MNLHVVKMKLSVSVLITY.....TNINKVANEESTLEHTKDEL 524		7	1034	38.3	Sequence 1, Appli
Scoring table:	BLOSUM62		8	999	37.0	Sequence 1068, AP
	Gapop 10.0 , Gapext 0.5		9	999	37.0	Sequence 1025, AP
Searched:	6959266 seqs, 1168006243 residues		10	999	37.0	Sequence 590, AP
Total number of hits satisfying chosen parameters:	6959266		11	999	37.0	Sequence 4, Appli
Minimum DB seq length: 0			12	999	37.0	Sequence 13, Appli
Maximum DB seq length: 2000000000			13	999	37.0	Sequence 2, Appli
Post-processing: Minimum Match 0%			14	999	37.0	Sequence 84, Appli
	Maximum Match 1.00%		15	999	37.0	Sequence 24, Appli
Listing first 45 summaries			16	999	37.0	Sequence 1001-054-24
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	25: /cggn_6/prodata/1/paa/US101_COMB.pep:*		42	999	37.0	Sequence 84-84-84
	26: /cggn_6/prodata/1/paa/US102_COMB.pep:*		43	999	37.0	Sequence 84-84-84
	27: /cggn_6/prodata/1/paa/US103_COMB.pep:*		44	999	37.0	Sequence 84-84-84
	28: /cggn_6/prodata/1/paa/US104_COMB.pep:*		45	999	37.0	Sequence 84-84-84
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	30: /cggn_6/prodata/1/paa/US106_COMB.pep:*					; GENERAL INFORMATION:
	31: /cggn_6/prodata/1/paa/US107_COMB.pep:*					; APPLICANT: Iwamoto, Mitsutomi; Jung, Sang-Kee
	32: /cggn_6/prodata/1/paa/US108_COMB.pep:*					; TITLE OF INVENTION: NOVEL PROTEIN, ITS GENE, REAGENTS FOR INDUCING
	33: /cggn_6/prodata/1/paa/US109_COMB.pep:*					; TITLE OF INVENTION: APOTOPSIS, AND ANTICANCER AGENTS
	34: /cggn_6/prodata/1/paa/US110_COMB.pep:*					; FILE REFERENCE: 4703/OF214
	35: /cggn_6/prodata/1/paa/US111_COMB.pep:*					; CURRENT APPLICATION NUMBER: US-10-644-142
	36: /cggn_6/prodata/1/paa/US60_COMB.pep:*					; CURRENT FILING DATE: 2003-08-20
	37: /cggn_6/prodata/1/paa/US60_COMB.pep:*					; PRIOR APPLICATION NUMBER: US-09-230-388
						; PRIOR FILING DATE: 1999-01-22
						; PRIOR APPLICATION NUMBER: PCT/JP98/02261
						; PRIOR FILING DATE: 1999-05-22
						; SOFTWARE: PatentIn Ver. 2.0
						; LENGTH: SEQ ID NOS: 2
						; SEQ ID NO 1
						; TYPE: PT

## ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Organism: Scomber japonicus  
us-10-644-142-1

Query Match 100.0%; Score 2703; DB 32; Length 524;  
Best Local Similarity 100.0%; Pred. No. 1..le-246;  
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNLHVVKWLSSVSVLITLYSHTVALSLXEHLLADCLDKDYLQTLQDNLGLPHINTSH 60  
Db 1 MNLHVVKWLSSVSVLITLYSHTVALSLXEHLLADCLDKDYLQTLQDNLGLPHINTSH 60

Qy 61 HVIIVGAGMAGLTAAKLIQDAGHTVTILEANDRVGGRVETRVTNEKEGWAEMGAMRISS 120  
Db 61 HVIIVGAGMAGLTAAKLIQDAGHTVTILEANDRVGGRVETRVTNEKEGWAEMGAMRISS 120

Qy 121 HRIQWFTYKLGIVEMNEFVMTDDNTFTLVNGYRERTYVQENPDVILKYNSSESEKGISAD 180  
Db 121 HRIQWFTYKLGIVEMNEFVMTDDNTFTLVNGYRERTYVQENPDVILKYNSSESEKGISAD 180

Qy 181 DLDRLAQKVKEEVEANGCKAALKEVYRSKEYLKEEGGLSPGAQMIGDLINQSILMY 240  
Db 181 DLDRLAQKVKEEVEANGCKAALKEVYRSKEYLKEEGGLSPGAQMIGDLINQSILMY 240

Qy 181 TALSEMIYDQADYNSVTYHEVGGSDILPEAFLSVJDPVILLNSKVHROSDKGVTVS 300  
Db 181 TALSEMIYDQADYNSVTYHEVGGSDILPEAFLSVJDPVILLNSKVHROSDKGVTVS 300

Qy 301 YQTGNESSLMDLSADIIVLVTATAAKALFDIDFPPLSISKMEALRSVHYDSSTKILLTFRD 360  
Db 301 YQTGNESSLMDLSADIIVLVTATAAKALFDIDFPPLSISKMEALRSVHYDSSTKILLTFRD 360

Qy 301 YQTGNESSLMDLSADIIVLVTATAAKALFDIDFPPLSISKMEALRSVHYDSSTKILLTFRD 360

Qy 181 DLDRLAQKVKEEVEANGCKAALKEVYRSKEYLKEEGGLSPGAQMIGDLINQSILMY 240  
Db 181 DLDRLAQKVKEEVEANGCKAALKEVYRSKEYLKEEGGLSPGAQMIGDLINQSILMY 240

Qy 241 TALSEMIYDQADYNSVTYHEVGGSDILPEAFLSVJDPVILLNSKVHROSDKGVTVS 300  
Db 241 TALSEMIYDQADYNSVTYHEVGGSDILPEAFLSVJDPVILLNSKVHROSDKGVTVS 300

Qy 421 ELALRDLAKIHGEQWDKCTGVIVKWKNSADPSUGAFAFLPTPYQHLEYAQELPSSSEGVRH 480  
Db 421 ELALRDLAKIHGEQWDKCTGVIVKWKNSADPSUGAFAFLPTPYQHLEYAQELPSSSEGVRH 480

Qy 421 ELALRDLAKIHGEQWDKCTGVIVKWKNSADPSUGAFAFLPTPYQHLEYAQELPSSSEGVRH 480

Qy 301 YQTGNESSLMDLSADIIVLVTATAAKALFDIDFPPLSISKMEALRSVHYDSSTKILLTFRD 360  
Db 301 YQTGNESSLMDLSADIIVLVTATAAKALFDIDFPPLSISKMEALRSVHYDSSTKILLTFRD 360

Qy 361 KFWEDDGIRGKSTITDGFPSRYIYPSSHFTNETIGVLASYTWSDELLFGASDEELK 420  
Db 361 KFWEDDGIRGKSTITDGFPSRYIYPSSHFTNETIGVLASYTWSDELLFGASDEELK 420

RESULT 3  
US-10-645-094-1

Sequence 1, Application US/10645094  
GENERAL INFORMATION:  
APPLICANT: Iwanoto, Mitsunori; Jung, Sang-Kee  
TITLE OF INVENTION: NOVEL PROTEIN, ITS GENE, REAGENTS FOR INDUCING  
APOTOSIS, AND ANTICANCER AGENTS  
FILE REFERENCE: 4703/0F214  
NUMBER OF SEQ ID NOS: 2  
CURRENT FILING DATE: 2003-08-21  
PRIOR APPLICATION NUMBER: US/10/645, 094  
PRIOR FILING DATE: 2001-07-24  
PRIOR APPLICATION NUMBER: US 09/912, 176  
PRIOR FILING DATE: 1999-01-22  
PRIOR APPLICATION NUMBER: PCT/JP98/02261  
PRIOR FILING DATE: 1998-05-22  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 1  
LENGTH: 524  
TYPE: PRT  
ORGANISM: Scomber japonicus  
US-10-645-094-1

Query Match 100.0%; Score 2703; DB 32; Length 524;  
Best Local Similarity 100.0%; Pred. No. 1..le-246;  
Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MNLHVVKWLSSVSVLITLYSHTVALSLXEHLLADCLDKDYLQTLQDNLGLPHINTSH 60

Qy 61 HVIIVGAGMAGLTAAKLIQDAGHTVTILEANDRVGGRVETRVTNEKEGWAEMGAMRISS 120  
Db 61 HVIIVGAGMAGLTAAKLIQDAGHTVTILEANDRVGGRVETRVTNEKEGWAEMGAMRISS 120

Qy 121 HRIQWFTYKLGIVEMNEFVMTDDNTFTLVNGYRERTYVQENPDVILKYNSSESEKGISAD 180  
Db 121 HRIQWFTYKLGIVEMNEFVMTDDNTFTLVNGYRERTYVQENPDVILKYNSSESEKGISAD 180

Qy 1 MNLHVVKWLSSVSVLITLYSHTVALSLXEHLLADCLDKDYLQTLQDNLGLPHINTSH 60  
Db 1 MNLHVVKWLSSVSVLITLYSHTVALSLXEHLLADCLDKDYLQTLQDNLGLPHINTSH 60

Qy	181 DILDLALOKYKEEVANGCKAALEKYDRYSYKEVLEEGGLSPGAVRIMIGDLNQEQQM 240	Qy	390 HTNETIGULLASYTWSDESLFLGASDEELKELALRDLAKITH--GEQWWDKCTGVVK 446
Db	181 DILDLALOKYKEEVANGCKAALEKYDRYSYKEVLEEGGLSPGAVRIMIGDLNQEQQM 240	Db	381 TSG--VGITA-YGIGDDANFQALDFKDCA DIVNDLSLHOPKEDQTFCPSPMQR 437
Qy	241 TALSEMIYDADVNDSVTYHEVTGGSDLLPEAFLSVLDPILLNSKVKHIRQSDKGIVVS 300	Qy	447 WSADPYSLGCAFALFTPYQHLEYAQELFSSEGRVHAGEHTAFPHAWIETSMKSAAIRATN 506
Db	241 TALSEMIYDADVNDSVTYHEVTGGSDLLPEAFLSVLDPILLNSKVKHIRQSDKGIVVS 300	Db	438 WSLDKYAMGGITTFPYQFHQSSEALTAFFKRIFXAGEHTAFPHAWIETSMKSAAIRATN 497
Qy	301 YQTGNESSIMLSDLSADIYLVTTAAKALFIDFDPLSISMEALRSVHDSDSTKILLTRD 360	Qy	507 INKVANEESTIETIKD 522
Db	301 YQTGNESSIMLSDLSADIYLVTTAAKALFIDFDPLSISMEALRSVHDSDSTKILLTRD 360	Db	498 VNRASENPSGITHLNSD 513
Qy	361 KFWEDDGIRGKSTITDGPSPRYIYPSSHFSHTNETIGULLASYTWSDESLFLGASDEELK 420		
Db	361 KFWEDDGIRGKSTITDGPSPRYIYPSSHFSHTNETIGULLASYTWSDESLFLGASDEELK 420		
Qy	421 ELALDLAKIHGEQWWDKCTGVVKWADPYSLGCAFALFTPYQHLEYAQELFSSEGRVH 480		
Db	421 ELALDLAKIHGEQWWDKCTGVVKWADPYSLGCAFALFTPYQHLEYAQELFSSEGRVH 480		
Qy	481 FAGEHTAFPHAWIETSMKSAAIRATNINVKVANEESTIETIKDEL 524		
Db	481 FAGEHTAFPHAWIETSMKSAAIRATNINVKVANEESTIETIKDEL 524		
Qy	481 FAGEHTAFPHAWIETSMKSAAIRATNINVKVANEESTIETIKDEL 524		
<b>RESULT 4</b>			
	US-09-791-537-143961	Query	Score 39.2%; Score 1059.5; DB 22; Length 516;
	Sequence 143961, Application US/09791537		Best Local Similarity 44.0%; Pred. No. 1 4e-90;
	GENERAL INFORMATION:		Matches 218; Conservative 94; Mismatches 171; Gaps 7;
	APPLICANT: Bionomix, Inc.		
	APPLICANT: Debe, Derek		
	APPLICANT: Danzer, Joseph		
	TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB		
	FILE REFERENCE: 26/1/210		
	CURRENT APPLICATION NUMBER: US/09/791,537		
	CURRENT FILING DATE: 2001-02-22		
	NUMBER OF SEQ ID NOS: 153055		
	SOFTWARE: PatentIn version 3.0		
	SEQ ID NO: 143961		
	LENGTH: 516		
	TYPE: PRT		
	ORGANISM: Crotalus adamanteus		
	US-09-791-537-143961		
<b>RESULT 5</b>			
	US-09-791-537-131193	Query	Score 39.2%; Score 1059.5; DB 22; Length 516;
	Sequence 131193, Application US/09791537		Best Local Similarity 44.0%; Pred. No. 1 4e-90;
	GENERAL INFORMATION:		Matches 218; Conservative 94; Mismatches 171; Gaps 7;
	APPLICANT: Bionomix, Inc.		
	APPLICANT: Debe, Derek		
	APPLICANT: Danzer, Joseph		
	TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB		
	FILE REFERENCE: 26/1/210		
	CURRENT APPLICATION NUMBER: US/09/791,537		
	CURRENT FILING DATE: 2001-02-22		
	NUMBER OF SEQ ID NOS: 153055		
	SOFTWARE: PatentIn version 3.0		
	SEQ ID NO: 143961		
	LENGTH: 516		
	TYPE: PRT		
	ORGANISM: Crotalus atrox		
	US-09-791-537-143961		
<b>Query Match</b>			
	39.3% Score 1063.5; DB 22; Length 516;		
	Best Local Similarity 44.0%; Pred. No. 6e-91;		
	Matches 218; Conservative 96; Mismatches 169; Indels 13; Gaps 7;		
	DB 203 EYLLKBNLSPGAVIDNGDLINEQSYVSPIESLKHDDIGYERKDEIVGGMDOLPTS 262		
Qy	33 LADCLDEDIYDTLQLTLQNLPHINTSHVVTVAGAGLTAALKLQDAHTGTVTILEAND 92	Qy	153 RERTYYVQENPDVLYKVNVESEKGISADDLDRALOKYKEEVANGCKAALEKYDRYSVK 212
Db	25 LEBCPREDYEEPLEIAKNGLPLQNLPHINTSHVVTVAGAGLTAALKLQDAHTGTVTILEAND 92	Db	143 RKVRREVYKNNPGLLEPVKPBSEEGKSAAQLYVESLRVKELKRTNCKYLQDLYSTK 202
Qy	93 RVGGRVETYNEKEGWWEMGMARISSHRIVYQWFKVKGIVMNEFYMDDNTFYLVNGV 152	Qy	213 EYLKEFGGLSPGAVIDNGDLINEQSYVSPIESLKHDDIGYERKDEIVGGSDLJPEA 272
Db	85 RVGGRVTRYR--KRDWANLGPMLPRLPTHRYREYKFDLKLNEFQDENENAWYFKNI 142	Db	203 EYLLKBNLSPGAVIDNGDLINEQSYVSPIESLKHDDIGYERKDEIVGGSDLJPEA 272
Qy	153 RERTYYVQENPDVLYKVNVESEKGISADDLDRALOKYKEEVANGCKAALEKYDRYSVK 212	Qy	273 FLSVL--DVPILLNSKVKHIRQSDKGIVYVSTQGNESIQLSDAIVLVTTAKALFI 329
Db	143 RKVRREVYKNNPGLLEPVKPBSEEGKSAAQLYVESLRVKELKRTNCKYLQDLYSTK 202	Db	263 MYEAIKEKVQHFNARVIEQDNDREATVYQTSANEM - SVTAAYVIVCTTSRAARI 320
Qy	213 EYLKEFGGLSPGAVIDNGDLINEQSYVSPIESLKHDDIGYERKDEIVGGSDLJPEA 272	Qy	330 DFDPPLSISKMEALSRYHYDSTSCKLILFRDKFWEEDGIRGGKSITDGPSRYIYPSHSF 389
Db	203 EYLLKBNLSPGAVIDNGDLINEQSYVSPIESLKHDDIGYERKDEIVGGMDOLPTS 262	Db	321 KFEPPLPPKKKAHALRSVHYRGTKPLTCFKFWEDDGHGKSTRDLSRFIYPMHNF 380
Qy	273 FLSVL--DVPILLNSKVKHIRQSDKGIVYVSTQGNESIQLSDAIVLVTTAKALFI 329	Qy	390 HTNETIGULLASYTWSDESLFLGASDEELKELALRDLAKITH--GEQWWDKCTGVVK 446
Db	263 MYEAIKEKVQHFNARVIEQDNDREATVYQTSANEM - SVTAAYVIVCTTSRAARI 320	Db	381 TSG--VGITA-YGIGDDANFQALDFKDCA DIVNDLSLHOPKEDQTFCPSPMQR 437
Qy	330 DFDPPLSISKMEALSRYHYDSTSCKLILFRDKFWEEDGIRGGKSITDGPSRYIYPSHSF 389	Qy	447 WSADPYSLGCAFALFTPYQHLEYAQELFSSEGRVHAGEHTAFPHAWIETSMKSAAIRATN 506
Db	321 KFEPPLPPKKKAHALRSVHYRGTKPLTCFKFWEDDGHGKSTRDLSRFIYPMHNF 380	Db	438 WSLDKYAMGGITTFPYQFHQSSEALTAFFKRIFXAGEHTAFPHAWIETSMKSAAIRATN 497
Qy	507 INKVANEESTIETIKD 522	Qy	507 INKVANEESTIETIKD 522
Db	498 VNRASENPSGITHLNSD 513	Db	498 VNRASENPSGITHLNSD 513

RESULT 6  
US-09-791-537-143903  
GENERAL INFORMATION:  
APPLICANT: Bionomix, Inc.  
APPLICANT: Debe, Derek  
APPLICANT: Danzer, Joseph  
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROBIN FAMILIES AND FAMILY MEMBE  
FILE REFERENCE: 2611/210  
CURRENT APPLICATION NUMBER: US/09/791,537  
CURRENT FILING DATE: 2001-04-22  
NUMBER OF SEQ ID NOS: 153055  
SOFTWARE: PatentIn version 3.0  
LENGTH: 630  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-791-537-143903

Query Match 38.3%; Score 1034; DB 22; Length 630;  
Best Local Similarity 43.5%; Pred. No. 5.3e-88;  
Matches 212; Conservative 100; Mismatches 163; Indels 12; Gaps 6;

Query 26 ALSLKEHLADCLEDKDYDTLQLDNLPHINTSHVNTVAGAGLTAKKLQDAGHTY 85  
Db 25 AASSLNPIEKCMEDDYEQLLKVVTLGLNRTSKPQKVNVYAGVGLVAARKMLSDAGHKV 84

Query 86 TILEANDRVRGGRVETYRNKEGYAEMGAMRIPSSHRIVQMFVKLGVEENEFVMTDDNT 145  
Db 85 TILEADNRIGRIFFRDEKTGWICELGAMRMPSSHRLHKLCRTLGLNLQTQFYDENT 144  
Db 85 WTEVHNVKLNRVYVEMPERGLGVNNRERGHSPDIYQMLNAFKDLKALGCKKAMNK 204

Query 146 FYLVNGVRERTYVQENPDVLKYNNSESEKGISADDLDRALQKTYKEVANGCKAALEK 205  
Db 145 WTEVHNVKLNRVYVEMPERGLGVNNRERGHSPDIYQMLNAFKDLKALGCKKAMNK 204

Query 206 YDRYSVKEYLKEEGGLSPGAVRMIDQADVNDSTYHEVTGG 265  
Db 205 FNKHTILEYLLEEGNLSRPAVQVLQDMSREGFFYLSDVMSRFLRYSRIVGG 264

Query 266 SDLPPAFLSVLDVILLNSKVKHTRQSDKGKVIVSQTGNBESSMLDSADIVLVTTAKA 325  
Db 265 WDLRPLALLSSLGALLNAPVVSITQGRNDVRHIALTSHSE-KTLDADVVLITASGPA 323

Query 326 ALFIDFDPLSISKMEALRSVHYDSTSKILLFRDKFWEDDGIRGGSITDGPSVSYIYP 385  
Db 324 LQRITFSPLTRKQEARALHYVAASKVELSRPRPWHEELEGHSNTDRPSLIFYP 383

Query 206 YDRYSVKEYLKEEGGLSPGAVRMIDQADVNDSTYHEVTGG 265  
Db 205 FNKHTILEYLLEEGNLSRPAVQVLQDMSREGFFYLSDVMSRFLRYSRIVGG 264

Query 266 SDLPPAFLSVLDVILLNSKVKHTRQSDKGKVIVSQTGNBESSMLDSADIVLVTTAKA 325  
Db 265 WDLRPLALLSSLGALLNAPVVSITQGRNDVRHIALTSHSE-KTLDADVVLITASGPA 323

Query 386 SHSFPTNETGIVLASYTWDESLFLGASDEELRKLARDLAKHGE--QVMRKCTGV 442  
Db 384 ARGEGS---LILASYTWSDAAAFPGLSTQDTRVLQDVAAHGPPVFLWDG-RGV 437

Query 443 IVKKWSADPYSLGAFALFTPYQHLEYAQELFSS-GRVHFAGEHTAFAHWIETSMKSAI 501  
Db 384 ARGEGS---LILASYTWSDAAAFPGLSTQDTRVLQDVAAHGPPVFLWDG-RGV 437

Query 443 IVKKWSADPYSLGAFALFTPYQHLEYAQELFSS-GRVHFAGEHTAFAHWIETSMKSAI 501  
Db 384 ARGEGS---LILASYTWSDAAAFPGLSTQDTRVLQDVAAHGPPVFLWDG-RGV 437

Query 502 RAATNIN 508  
Db 497 RAAVRIN 503

RESULT 7  
US-09-938-795A-1  
GENERAL INFORMATION:  
APPLICANT: CHU, CHARLES CHIVIAN  
APPLICANT: CHAVAN, SANGBETA S.  
APPLICANT: MASON, JAMES M.  
TITLE OF INVENTION: HUMAN INTERLEUKIN-FOUR INDUCED PROTEIN  
FILE REFERENCE: LIJ-9000-US  
CURRENT APPLICATION NUMBER: US/09/938,795A

PCT-US02-08123-1068

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 9.3e-85; Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

Qy 3 LHVKWKLSVSVLITYSHT-VALSLKEHLADCLEDKDPTLQLTDLNGLPHINTSHH 61

Db 6 LHL---LVLPILLSLVASQDWKAERSQDPFEKCMQDPYBQLKVTWGLNRTLKQR 61

Qy 62 VVIVGAGMAGLTAAKLIQDAGHTVTILEANDRVRGGRVETYRNKEGYAEMGAMRIPSSH 121

Db 62 VIVVGAGVAGLVAAKVLSDAHGKVTLLEADNRIGRIFTYRDQNTGWIGELGMARMPSSH 121

Qy 122 RIVQWFVKKLGIVEMNEFVMTDDNTFLYNGRERITYVQENPDVLKYNSSEKGISADD 181

Db 122 RILHKLCQGLNLTKPQDXNTWTEVEHKLRLNVYVERPEKLGYALRPOEKGHSPEC 181

Qy 182 LLDRALOKVKEEVAANGCKAALEKTVSYKEYLKEEGGLSPGAVMIGDLNNEOSLIMYT 241

Db 182 IYQMAJNOAQLDALKALGCRKAMKKFETHTLJELBLGEGNLNSRPAVQLGDSEDGFYL 241

Qy 242 ALSEMIDYQADVNDSUTYHEVYGSDLIPAEFLSLVDPLILNSKVKHIROSDKGTVSY 301

Db 242 SFAELRAHSCLSDRLQYSRIVGGWDLPLRALSLSGLVLNAPVYAMTOPHDYHVQI 301

Qy 302 QTGNES-SLMLDLSADIIVLVTTAKAALFIDDPPLTSKMEALSRYHDSSTRKILLTFRD 360

Db 302 ETSPPARNLKVTKADVLLTAGSPAVKRITFSPLPRHMQEAIRLHYVPATKFLSFRR 361

Qy 361 KFWDDGIRGKKSITDGPSSRYTYPSSHFHTNETIGVLLASLASTWSDESLLFLGASDEBK 420

Db 361 DDWTVPYGRIVFAGHTAYPHGWETAVKSALARAIKIN 508

Qy 362 PFWREEHLEGGNSNTDRSRMIFYP----PPREGALLLASTWSDAAAAGFLSREBAL 416

Db 362 PFWREEHLEGGNSNTDRSRMIFYP----PPREGALLLASTWSDAAAAGFLSREBAL 416

Qy 421 ELALRDLAKING--EQWWDIKCTGVVKKWSADPSUGAFALFTPYQHLEYAQELFSS- 476

Db 417 RLALDDVAAHLGPVVRQLWDG-TGV-VKRWADQHSCQGFVQQP-----ALWQTEK 466

Qy 477 -----GRVHFAAGENTFAFPHWIETSMKSAITRAATMIN 508

Db 467 DDWTVPYGRIVFAGHTAYPHGWETAVKSALARAIKIN 505

RESULT 9 PCT-US02-08278-1025

Sequence 1025, Application PC/TUS0208278

GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc.

TITLE OF INVENTION: Human Secreted Proteins

FILE REFERENCE: PS905CCT

CURRENT APPLICATION NUMBER: PCT/US02/09785

CURRENT FILING DATE: 2002-03-19

PRIOR APPLICATION NUMBER: US 60/331,287

PRIOR FILING DATE: 2001-11-13

PRIOR APPLICATION NUMBER: US 60/306,171

PRIOR FILING DATE: 2001-07-19

PRIOR APPLICATION NUMBER: US 60/277,340

PRIOR FILING DATE: 2001-03-21

NUMBER OF SEQ ID NOS: 1130

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 590

LENGTH: 567

TYPE: PRT

ORGANISM: Homo sapiens

PCT-US02-09785-590

Query Match 37.0%; Score 999; DB 1; Length 567;

Best Local Similarity 41.8%; Pred. No. 9.3e-85; Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

Qy 3 LHVKWKLSVSVLITYSHT-VALSLKEHLADCLEDKDPTLQLTDLNGLPHINTSHH 61

Db 6 LHL---LVLPILLSLVASQDWKAERSQDPFEKCMQDPYBQLKVTWGLNRTLKQR 61

Qy 62 VVIVGAGMAGLTAAKLIQDAGHTVTILEANDRVRGGRVETYRNKEGYAEMGAMRIPSSH 121

Db 62 VIVVGAGVAGLVAAKVLSDAHGKVTLLEADNRIGRIFTYRDQNTGWIGELGMARMPSSH 121

Qy 122 RIVQWFVKKLGIVEMNEFVMTDDNTFLYNGRERITYVQENPDVLKYNSSEKGISADD 181

Db 122 RILHKLCQGLNLTKPQDXNTWTEVEHKLRLNVYVERPEKLGYALRPOEKGHSPEC 181

Qy	182 LLDRALQKVKEEVEANGKAALEKYDRIESVKEYLKEEGGLSPGAVRMIGDLINNEQLSMLYT 241	Db	242 SFAEAIRAHSCLSLDLQYSRIVGGNDLLPRALESSLGVLNNAVVAMTQGPHDVHVQI 301
Db	182 IYOMAHLQKDLKALQKCRANKKFERHTLLEYLGEGNMSEDFFYL 241	Qy	302 OTGNES-SLMDSLADIVLVTTAKAALFIDFPPLTSKMEALRHYDSTSSTKILLTFRD 360
Qy	242 ALSEMIVYQADWNSVTYHEVTGSDILPEAFSLVDPILLNSKVKHROSDFGVTVSY 301	Db	302 ETSPARNLXVLAQVLLTASGPVAKRTTESPPRHMDEALRLHYVATKVPUSFR 361
Db	242 SPAEAIRAHSCLSLDLQYSRIVGGNDLLPRALESSLGVLNNAVPTVAMTQGPHDVHVQI 301	Qy	361 KFWEDDGIRGKKSITDGSRYIYDHSFSHTNETIVGLASYTWSDESLFLGASDEELK 420
Qy	302 OTGNES-SLMDSLADIVLVTTAKAALFIDFPPLTSKMEALRHYDSTSSTKILLTFRD 360	Db	362 PFWREHIEGSHNTDTPSMIFY-----PPREGAILASYTWDAAAFAGLSREAL 416
Db	302 ETSPARNLXVLAQVLLTASGPVAKRTTESPPRHMDEALRLHYVATKVPUSFR 361	Qy	421 ELALRDLAKIHG---EQWVKRCTGVTKWMSADPSLGAFAFLTYQHLEYAQELEFSSE- 476
Qy	361 KFWEDDGIRGKKSITDGSRYIYDHSFSHTNETIGVILASYTWSDESLFLGASDEELK 420	Db	417 RLALDDVAALHGPPVTRLWDG-TGV-VKRMWAEDQISQGGFVQOPP-----ALWOTEK 466
Db	362 PFWREHIEGSHNTDTPSMIFY-----PPREGAILASYTWSDESLFLGASDEELK 420	Qy	477 -----GRVHFAGEHTAFAPHAWIETSMKSAIRATNN 508
Qy	421 ELALRDLAKIHG---EQWVKRCTGVTKWMSADPSLGAFAFLTYQHLEYAQELEFSSE- 476	Db	467 DDWTVPYGRITYFAGGHTAYDHGWVSTAVKSALRAAIKIN 505
Db	417 RLALDDVAALHGPPVTRLWDG-TGV-VKRMWAEDQISQGGFVQOPP-----ALWOTEK 466		
Qy	477 -----GRVHFAGEHTAFAPHAWIETSMKSAIRATNN 508		RESULT 12 US-09-882-636-13
Db	467 DDWTVPYGRITYFAGGHTAYDHGWVSTAVKSALRAAIKIN 505		; Sequence 13, Application US/09882636
Qy	477 -----GRVHFAGEHTAFAPHAWIETSMKSAIRATNN 508		; GENERAL INFORMATION:
Db	467 DDWTVPYGRITYFAGGHTAYDHGWVSTAVKSALRAAIKIN 505		; APPLICANT: Botstein, David
			; APPLICANT: Goddard, Audrey
			; APPLICANT: Gurney, Austin L.
			; APPLICANT: Hillian, Kenneth
			; APPLICANT: Lawrence, David A.
			; APPLICANT: Roy, Margaret, Ann
			; APPLICANT: Wood, William J.
			; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
			; FILE REFERENCE: P509R1C1
			; CURRENT APPLICATION NUMBER: US/09/882,636
			; CURRENT FILING DATE: 2003-06-14
			; PRIOR APPLICATION NUMBER: 60/113,296
			; PRIOR FILING DATE: December 22, 1998
			; PRIOR APPLICATION NUMBER: 60/112,850
			; PRIOR FILING DATE: December 16, 1998
			; PRIOR APPLICATION NUMBER: 60/107,783
			; PRIOR FILING DATE: November 10, 1998
			; PRIOR APPLICATION NUMBER: 60/088,742
			; PRIOR FILING DATE: June 10, 1998
			; PRIOR APPLICATION NUMBER: 60/086,414
			; PRIOR FILING DATE: May 22, 1998
			; PRIOR APPLICATION NUMBER: 60/083,500
			; PRIOR FILING DATE: April 29, 1998
			; PRIOR APPLICATION NUMBER: 60/082,767
			; PRIOR FILING DATE: April 23, 1998
			; PRIOR APPLICATION NUMBER: 60/074,086
			; PRIOR FILING DATE: February 9, 1998
			; PRIOR APPLICATION NUMBER: 60/070,440
			; PRIOR FILING DATE: January 5, 1998
			; PRIOR APPLICATION NUMBER: 60/069,873
			; PRIOR FILING DATE: December 17, 1997
			; PRIOR APPLICATION NUMBER: 60/069,702
			; PRIOR FILING DATE: December 16, 1997
			; PRIOR APPLICATION NUMBER: 60/069,694
			; PRIOR FILING DATE: December 16, 1997
			; PRIOR APPLICATION NUMBER: 60/069,696
			; PRIOR FILING DATE: December 16, 1997
			; PRIOR APPLICATION NUMBER: 60/066,772
			; PRIOR FILING DATE: November 24, 1997
			; PRIOR APPLICATION NUMBER: 60/032,705
			; PRIOR FILING DATE: December 12, 1996
			; PRIOR APPLICATION NUMBER: PCT/US00/12678
			; PRIOR FILING DATE: December 1, 2000
			; PRIOR APPLICATION NUMBER: 09/709,238
			; PRIOR FILING DATE: September 18, 2000
			; PRIOR APPLICATION NUMBER: 09/665,350
			; PRIOR FILING DATE: September 18, 2000
			; PRIOR APPLICATION NUMBER: PCT/US00/23522

PRIOR FILING DATE: August 23, 2000  
 PRIOR APPLICATION NUMBER: PCT/US00/14941  
 PRIOR FILING DATE: May 30, 2000  
 PRIOR APPLICATION NUMBER: PCT/US00/13705  
 PRIOR FILING DATE: May 17, 2000  
 PRIOR APPLICATION NUMBER: PCT/US00/08439  
 PRIOR FILING DATE: March 30, 2000  
 PRIOR APPLICATION NUMBER: PCT/US00/05841  
 PRIOR FILING DATE: March 2, 2000  
 PRIOR APPLICATION NUMBER: PCT/US00/05004  
 PRIOR FILING DATE: February 24, 2000  
 PRIOR APPLICATION NUMBER: PCT/US00/04414  
 PRIOR FILING DATE: February 22, 2000  
 PRIOR APPLICATION NUMBER: PCT/US00/04341  
 PRIOR FILING DATE: February 18, 2000  
 PRIOR APPLICATION NUMBER: PCT/US00/04342  
 PRIOR FILING DATE: February 10, 2000  
 PRIOR APPLICATION NUMBER: PCT/US00/04800  
 PRIOR FILING DATE: January 10, 2000  
 PRIOR APPLICATION NUMBER: PCT/US00/30095  
 PRIOR FILING DATE: December 16, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/28865  
 PRIOR FILING DATE: December 1, 1999  
 PRIOR APPLICATION NUMBER: 09/423,844  
 PRIOR FILING DATE: November 12, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/28301  
 PRIOR FILING DATE: December 1, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/28410  
 PRIOR FILING DATE: November 30, 1999  
 PRIOR APPLICATION NUMBER: 09/403,297  
 PRIOR FILING DATE: October 18, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/21090  
 PRIOR FILING DATE: September 15, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/20111  
 PRIOR FILING DATE: September 1, 1999  
 PRIOR APPLICATION NUMBER: 09/380,137  
 PRIOR FILING DATE: August 25, 1999  
 PRIOR APPLICATION NUMBER: 09/380,138  
 PRIOR FILING DATE: August 25, 1999  
 PRIOR APPLICATION NUMBER: 09/380,139  
 PRIOR FILING DATE: August 25, 1999  
 PRIOR APPLICATION NUMBER: 09/367,206  
 PRIOR FILING DATE: August 9, 1999  
 PRIOR APPLICATION NUMBER: 09/369,028  
 PRIOR FILING DATE: August 4, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/12252  
 PRIOR FILING DATE: June 2, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/08847  
 PRIOR FILING DATE: April 23, 1999  
 PRIOR APPLICATION NUMBER: 09/284,404  
 PRIOR FILING DATE: April 23, 1999  
 PRIOR APPLICATION NUMBER: 09/284,291  
 PRIOR FILING DATE: April 12, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/05028  
 PRIOR FILING DATE: March 8, 1999  
 PRIOR APPLICATION NUMBER: 09/354,311  
 PRIOR FILING DATE: March 3, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/00106  
 PRIOR FILING DATE: January 5, 1999  
 PRIOR APPLICATION NUMBER: 09/218,517  
 PRIOR FILING DATE: December 22, 1998  
 PRIOR APPLICATION NUMBER: 09/216,021  
 PRIOR FILING DATE: December 16, 1998  
 PRIOR APPLICATION NUMBER: PCT/US98/25108  
 PRIOR FILING DATE: December 1, 1998  
 PRIOR APPLICATION NUMBER: PCT/US98/19330  
 PRIOR APPLICATION NUMBER: 09/065,275  
 PRIOR FILING DATE: April 23, 1998  
 PRIOR APPLICATION NUMBER: 08/987,902  
 PRIOR FILING DATE: December 10, 1997  
 PRIOR APPLICATION NUMBER: PCT/US97/22228  
 PRIOR FILING DATE: December 5, 1997

; NUMBER OF SEQ ID NOS: 113  
; SEQ ID NO 13  
; LENGTH: 567  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-09-882-636-13

Query Match 37.0%; Score 999; DB 23; Length 567;  
Best Local Similarity 41.0%; Pred. No. 9.3e-85;  
Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

Query 3 LHVKWKLSVSVLTLTYYSH-VALSLKEHLADCLEDKDYDTLLOTLGLPHINTSHH 61  
Db 6 LHL---LVLPVILSVAQDWAERSQDPFEKCMQDPDYEQLLKVTVGLNRTLKPCR 61

Query 62 VVIVGAGMAGLTAAKULQDAGHTYTLLEANDRVCGRVETYNEKEKSYAENGAMRIPSSH 121  
Db 62 VVIVGAGVAGLVAQKVLSLDAGHKVTLLEADNRIGRIFTYDQNTZWIGJGMRMPSHH 121

Query 122 RIVQWFVKKGVMONBFVMTDDNTFLVLNGYRERTTYVQENPDLKVNVSSEKGNSADD 181  
Db 122 RILHKUCQGLGLNLTKFTQDKNTEVHEVYLKRNLYVEKPEKLGYALRQEKGHSPED 181

Query 182 LLDRALQKVKEBEVANGCKAALEKTDYRSKEYLKEBEGGLSPGAVRMIGDLNEQSMLYT 241  
Db 182 IYQMANLNQALKDQLKALGCKAMKKFBRTHLLEYLGEGLNLSRPVQQLGDMSEDGFYFL 241

Query 242 ALSEMYDOAVNDTSVITYHEVYGGSIDLPEFLSLVDVPLILNSKVKHIRQSDKGIVTYSV 301  
Db 242 SFAEALRAHSCSLRQLQYSRIVGWDPLRALLSSLSGLVLLNAPVAMTOGPHDYHVQI 301

Query 302 QTGNES-SLMDSLSDAVLVTTTAKAALFIDDPPLSISKMBALRYHYDSSTS KILLTFRD 360  
Db 302 ETSPPARNLKWLKDADVVLATASGPVKRITPSPPPLPRHMQEALRLRHYPATVKFLSFR 361

Query 361 KFWEDDGIRGKGSITDGPSTYIYPSHSFHNETICVLLASYTWSDESLFLFGASDELK 420  
Db 362 PFWREHIEGHNSNTDRPSRMIFYP----PREGALLASYTWSDAAAAGLSSREAL 416

Query 421 ELALRDIAKTHG--EQWQDKCTGTIVKKWSSADPYSLGAFALFTYQHLEYAQEFSSE- 476  
Db 417 RLALDDVAALHGPVVRQLWDS-TGV-KVRAWBQDQSQQGPVVQPP-----ALWQTEK 466

Query 477 -----GRVHPAGEHTAPPHAWITSMSKAIRATINN 508  
Db 467 DDWTVPYGRITYFAGGHTAYPHGWVETAVKSALARAIKIN 505

RESULT 13  
US-09-938-795A-2  
; Sequence 2, Application US/09938795A  
; GENERAL INFORMATION:  
; APPLICANT: CHU, CHARLES CHIYUAN  
; APPLICANT: CHAVAN, SANGEETA S.  
; APPLICANT: MASON, JAMES M.  
; TITLE OF INVENTION: HUMAN INTERLEUKIN-FOUR INDUCED PROTEIN  
; FILE REFERENCE: LIJ-9600-US  
; CURRENT APPLICATION NUMBER: US/09/938,795A  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: 60/227,818  
; PRIOR FILING DATE: 2000-08-25  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 567  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-938-795A-2

Query Match 37.0%; Score 999; DB 24; Length 567;  
Best Local Similarity 41.0%; Pred. No. 9.3e-85;  
Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

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 Db 122 RILHKLCGGLGNLTKEFYDQNTTWETHEVLRNRYVEKPEKUGYALRQEKGHSIPED 181  
 Qy 182 LLDRALOKVKEEYANGKAALEKYDRYSVKEYLKEEGLSPGAVRMGDLINNEQSMLYT 241  
 Db 182 TYOMALQALKALGCRKAMKKFERTTLEYLGSGNISRPAYQOLGDYMDSEGGFLY 241  
 Qy 242 ALSEMITYOADDYNDSYTHEVTCGSDLILPEAFSLVDPILLNSKVKHROSDFKGTVY 301  
 Db 242 SFAEALRAHSCLSDRLQYSRIVGWDLPRALLSLSGLVLELNAPVMTQPHDVHQI 301  
 Qy 302 CTGNES-SLMMLSADTVLVTCTAAKAALFIDFPPLSTKMPALRSVHDYDSSTKLLTFRD 360  
 Db 302 ETSPPARNLKVKRADVVLATASPRAKRTRHYPATKVFSLFRR 361  
 Qy 361 KFWEDEDSJRGGSXITSQPSRYYPPSHSFHNETIGVULASYTWSDESLFLGASDEELK 420  
 Db 362 PWREEHIEGGHSNTDRSRMFP----PREGAILLASYTWSAAAFAAGLSRREAL 416  
 Qy 421 ELALRDLAKING---EOWWDCTGTIVYRKWSADPSLGAFLPTPYOHLEYAQELFSS- 476  
 Db 417 RLADDVAHLGPVVRQLWDG-TGV-VKRWADQHSGGFVQQP-----ALWOTEK 466  
 Qy 477 -----GRVHFAGENTAAPHAWIETSMKSAIRAATNN 508  
 Db 467 DDWTVPYGRYFAGEHTAPHEWETAVSKALARAIKN 505

RESULT 14  
 US-09-946-374-84  
 Sequence 84, Application US/0946374

GENERAL INFORMATION  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, Christopher J.  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Hillan, Kenneth J.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Smith, Victoria  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumms, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2030P1C1  
 CURRENT APPLICATION NUMBER: US/09/946,374  
 CURRENT FILING DATE: 2001-05-04  
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; PRIOR FILING DATE: 1998-10-27

Query Match 37.0% Score 999; DB 24;
Best Local Similarity 41.8%; Pred. No. 9.3e-85;
Matches 217; Conservative 99; Mismatches 171;
Indels 32; Gaps 9;

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Db 6 LHL-----LVLPLTLLSLVASQDWKAERSQDPFEKCMQDPDVQLKLKVUTWGLNTRLKRQ 61

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Qy 242 ALSEMUYQADVNDSTYHBTGGSDOLPEAFLSVLDVPILLNSKVHIRQSDKGTVIVSY 301
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Qy 302 QTGNES-SLMDSLADIVLTATKAAFLIDDDPPLSTSJKMRLRSVHYDSSTKLJTFRD 360
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RESULT 15
US-10-001-054-24
Sequence 24, Application US/10001054
GENERAL INFORMATION:
; APPLICANT: Generitech, Inc.
; APPLICANT: Baker, Kevin
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Hebert, Carolyn
; APPLICANT: Henzel, William
; APPLICANT: Kabakoff, Rhona

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APPLICANT: Shelton, David  
 APPLICANT: Smith, Victoria  
 APPLICANT: Watanabe, Colin  
 APPLICANT: Wood, William

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH

FILE REFERENCE: P334R1CCT

CURRENT APPLICATION NUMBER: US/10/001,054

CURRENT FILING DATE: 2001-11-30

PRIOR APPLICATION NUMBER: 60/059114  
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 PRIOR FILING DATE: 2001-09-04

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; ORGANISM: Homo Sapien
us-10-001-054-24

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Query Match 37.0%; Score 999; DB 26; Length 567;

Best Local Similarity 41.8%; Pred. No. 9\_3e-85; Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

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3	2703	100.0	524	Sequence 1, Appli
4	1034	38.3	630	Sequence 2, Appli
5	999	37.0	567	Sequence 84, Appli
6	999	37.0	567	Sequence 24, Appli
7	999	37.0	567	Sequence 2, Appli
8	999	37.0	567	Sequence 476, App
9	999	37.0	567	Sequence 476, App
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11	999	37.0	567	Sequence 476, App

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Db	181 DLLRALQKVEEYANGCKAALEKDYDSKEYLKEEGLSPGAVMGDLNEQS1MY 240	301 YOTGNESSLMLPSADIVLWTTAKAALFLIDDPPLSISKMEALRSVHYDSSSTKILLTFRD 360
Qy	181 DLLRALQKVEEYANGCKAALEKDYDSKEYLKEEGLSPGAVMGDLNEQS1MY 240	361 KFWEDDGIRGKKSITDGPSPRVIYSSHFSHTNETCIVLLASYTWSDESLPFGASDBELK 420
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Qy	241 TALESEMYDOADVNDSVTYHETGGSDLLPEAFLSVYLDVPIILNSKVKHFRQSDKGIVS 300	361 KFWEDDGIRGKKSITDGPSPRVIYSSHFSHTNETCIVLLASYTWSDESLPFGASDBELK 420
Db	301 YOTGNESSLMLPSADIVLWTTAKAALFLIDDPPLSISKMEALRSVHYDSSSTKILLTFRD 360	421 ELARDLAKTHGEQWMDKCTGVIVKWSADPYSLGAFALFTPYQHLEYAQELFSSEGRVH 480
Qy	301 YOTGNESSLMLPSADIVLWTTAKAALFLIDDPPLSISKMEALRSVHYDSSSTKILLTFRD 360	421 ELARDLAKTHGEQWMDKCTGVIVKWSADPYSLGAFALFTPYQHLEYAQELFSSEGRVH 480
Db	361 KFWEDDGIRGKKSITDGPSPRVIYSSHFSHTNETCIVLLASYTWSDESLPFGASDBELK 420	481 PAGEHTAPHAWIETSMKSAIRATNINKVANEESTLIEHTKDEL 524
Qy	361 KFWEDDGIRGKKSITDGPSPRVIYSSHFSHTNETCIVLLASYTWSDESLPFGASDBELK 420	481 PAGEHTAPHAWIETSMKSAIRATNINKVANEESTLIEHTKDEL 524
Db	421 ELARDLAKTHGEQWMDKCTGVIVKWSADPYSLGAFALFTPYQHLEYAQELFSSEGRVH 480	RESULT 3 US-10-645-094-1 Sequence 1, Application US/10645094 Publication No. US20050191737A1
Qy	421 ELARDLAKTHGEQWMDCTGVIVKWNADPYSLGAFALFTPYQHLEYAQELFSSEGRVH 480	GENERAL INFORMATION: APPLICANT: Iwamoto, Mitsunori; Jung, Sang-Kee TITLE OF INVENTION: NOVEL PROTEIN, ITS GENE, REAGENTS FOR INDUCING TITLE OF INVENTION: APOTOSIS, AND ANTICANCER AGENTS FILE REFERENCE: 4703/0F214 CURRENT APPLICATION NUMBER: US/10/645,094 PRIORITY NUMBER: US 09/912,176 PRIOR FILING DATE: 2003-08-21 PRIOR APPLICATION NUMBER: US 09/912,176 PRIOR FILING DATE: 1999-01-22 PRIOR APPLICATION NUMBER: PCT/JP98/02261 PRIOR FILING DATE: 1998-05-22 NUMBER OF SEQ ID NOS: 2 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 1 LENGTH: 524 TYPE: PRT ORGANISM: Scomber japonicus US-10-645-094-1
Db	481 PAGEHTAPHAWIETSMKSAIRATNINKVANEESTLIEHTKDEL 524	Query Match 100.0%; Score 2703; DB 18; Length 524; Best Local Similarity 100.0%; Pred. No. 1..3e-216; Matches 524; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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Qy	481 PAGEHTAPHAWIETSMKSAIRATNINKVANEESTLIEHTKDEL 524	61 DUDRALQKVEEYANGCKAALEKDYDSKEYLKEEGLSPGAVMGDLNEQS1MY 240 Db 181 DUDRALQKVEEYANGCKAALEKDYDSKEYLKEEGLSPGAVMGDLNEQS1MY 240
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Qy	61 HVTIVGAGNGLTAALKLQDAUGHTVITILEANDRGGRVETYNEKEGYAENGAMRIPSS 120	121 HRTIVQFWFKLGEMNEFWMDDNTFTYLNGVRERTYVQENPDVKYNSSEKGS1AD 180 121 HRTIVQFWFKLGEMNEFWMDDNTFTYLNGVRERTYVQENPDVKYNSSEKGS1AD 180
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Qy	121 HRTIVQFWFKLGEMNEFWMDDNTFTYLNGVRERTYVQENPDVKYNSSEKGS1AD 180	241 TALESEMYDOADVNDSVTYHETGGSDLLPEAFLSVYLDVPIILNSKVKHFRQSDKGIVS 300 241 TALESEMYDOADVNDSVTYHETGGSDLLPEAFLSVYLDVPIILNSKVKHFRQSDKGIVS 300
Db	121 HRTIVQFWFKLGEMNEFWMDDNTFTYLNGVRERTYVQENPDVKYNSSEKGS1AD 180	301 YOTGNESSLMLPSADIVLWTTAKAALFLIDDPPLSISKMEALRSVHYDSSSTKILLTFRD 360
Qy	121 HRTIVQFWFKLGEMNEFWMDDNTFTYLNGVRERTYVQENPDVKYNSSEKGS1AD 180	
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 Result 5 US-09-938-795A-2  
 ; Sequence 2, Application US/09/938/795A  
 ; Publication No. US20030045688A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CHU, CHARLES CHIYUAN  
 ; APPLICANT: CHAVAN, SANGETA S.  
 ; APPLICANT: MASON, JAMES M.  
 ; TITLE OF INVENTION: HUMAN INTERLEUKIN-FOUR INDUCED PROTEIN  
 ; FILE REFERENCE: LIJ-9000-US  
 ; CURRENT APPLICATION NUMBER: US/09/938,795A  
 ; CURRENT FILING DATE: 2001-08-24  
 ; PRIORITY APPLICATION NUMBER: 60/227,818  
 ; PRIORITY FILING DATE: 2000-08-25  
 ; NUMBER OF SEQ ID NOS: 29  
 ; NUMBER OF SEQ ID NOS: 29  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO: 2  
 ; LENGTH: 630  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FILE REFERENCE: LIJ-9000-US  
 ; CURRENT APPLICATION NUMBER: US/09/938,795A  
 ; CURRENT FILING DATE: 2001-08-24  
 ; PRIORITY APPLICATION NUMBER: 60/227,818  
 ; PRIORITY FILING DATE: 2000-08-25  
 ; NUMBER OF SEQ ID NOS: 29  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO: 1  
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 ; Best Local Similarity 43.5%; Pred. No. 3.9e-77;  
 ; Matches 212; Conservative 100; Mismatches 163; Indels 12; Gaps 6;  
 ; Qy 26 ALSLKEHADCLEDKDYDTLQTLQDGHTAAKULQDGHTV 85  
 ; Db 25 AASSLNPEKCMDHDYEQQLKVVTGLNRNTSKPQKVYVVGAVGLVAAKMLSDAGHV 84  
 ; Qy 86 WTEVHNRYVEKMPPEKLGYNLNRRERGHSPEDIYQMLANKAPKDALKGCKKAMNK 204  
 ; Db 85 TILBADNIGGIFTFRBKIGWIGLAMRNPSSHLHKCUTRLQNSLQYHPTQYDENT 144  
 ; Qy 146 FYLVNGVERTYVQENPDVKYNSSESEKGSADDLDRALQKVKEEANGKAALEK 205  
 ; Db 145 WTEVHNRYVEKMPPEKLGYNLNRRERGHSPEDIYQMLANKAPKDALKGCKKAMNK 204  
 ; Qy 206 YDRYSVKEYLKEEGGLSGAVRMIGDLNEQSILMVTASEMITYQADVNDSVTYHVTGG 265  
 ; Db 205 FNKHTLLEYLLEBEGNLSPRAVQLGDYMESEGGFFYLSPAEALRAHCSDRLRSIVGG 264  
 ; Qy 266 SDLPLPEAFTSLVDPVILSKVTHIROSDFKGTVSYTGNESLSDLMSADIVLVTTAKA 325  
 ; Db 265 WDLPLRALSSLSGALLNAPVVSITQRNDVRVHTATSLABE-KTLDVFLTASPA 323  
 ; Qy 326 ALFDIFDPLSISKMEALRSVHYDSSTKILLTFRDKEWEDDGIRGSKSITDGPSPRYIYP 385  
 ; Db 324 LQRTFSPPLTKRQEALRHYVAASKVFLSRRPWEHEETIEGGHSNTDRPSRLIYFP 383  
 ; Qy 386 SHSFHNTETGULLASLFTWSDLSLFLFGASDEBLKLDIAKINGE--QWWDIKCTGV 442  
 ; Db 384 ARGEKS---LLASLTWSDAAAPFAGLSTDOTLRLVQDVAALHGPPVFRWLWDG-RGV 437  
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Result 6 US-09-946-374-84  
 ; Sequence 84, Application US/09/946374  
 ; Publication No. US20030073129A1  
 ; GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Denoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, Christopher J.  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Hillian, Kenneth J.  
 APPLICANT: James  
 APPLICANT: Paoni, Nicholas P.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Smith, Victoria  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2330P1C1  
 CURRENT APPLICATION NUMBER: US/09/946,374  
 CURRENT FILING DATE: 2001-08-04  
 PRIOR APPLICATION NUMBER: 60/098716  
 PRIOR FILING DATE: 1998-09-01  
 PRIOR APPLICATION NUMBER: 60/098723  
 PRIOR FILING DATE: 1998-09-01  
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 PRIOR FILING DATE: 1998-09-15  
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PRIOR FILING DATE: 1998-09-16  
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PRIOR FILING DATE: 1998-10-22  
PRIOR APPLICATION NUMBER: 60/105693  
PRIOR FILING DATE: 1998-10-26  
PRIOR APPLICATION NUMBER: 60/105694  
PRIOR FILING DATE: 1998-10-26  
PRIOR APPLICATION NUMBER: 60/105807

Query Match 37.0% Score 999; DB 10; Length 567;  
Best Local Similarity 41.8%; Prod. No. 2.8e-7; Mismatches 99; Indels 32; Gaps 9;

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Db 62 LLDRALQKVKEEVEANGKAALEKYDYSVKEYLGSGAVRMIDLINEQSMLYT 241  
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RESULT 7  
US-10-001-054-24  
Sequence 24, Application US/10001054  
Publication No. US002019220941  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Baker, Kevin  
APPLICANT: Goddard, Audrey  
APPLICANT: Gurney, Austin  
APPLICANT: Hebert, Carolyn  
APPLICANT: Henzel, William  
APPLICANT: Kabakoff, Rhona  
APPLICANT: Shelton, David  
APPLICANT: Smith, Victoria  
APPLICANT: Watanabe, Colin  
APPLICANT: Wood, William  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC  
TITLE OF INVENTION: CELL GROWTH  
FILE REFERENCE: P3034RIPCT  
CURRENT APPLICATION NUMBER: US/10/001,054  
CURRENT FILING DATE: 2001-11-30  
PRIOR APPLICATION NUMBER: 60/059114  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
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PRIORITY FILING DATE: 1999-07-20          PRIORITY APPLICATION NUMBER: PCT/US00/00376
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PRIORITY APPLICATION NUMBER: 60/187202          PRIORITY FILING DATE: 2000-02-18          PRIORITY APPLICATION NUMBER: PCT/US00/04341
PRIORITY FILING DATE: 2000-03-03          PRIORITY APPLICATION NUMBER: PCT/US00/04342
PRIORITY APPLICATION NUMBER: 60/209332          PRIORITY FILING DATE: 2000-02-18          PRIORITY APPLICATION NUMBER: PCT/US00/04342
PRIORITY FILING DATE: 2000-06-05          PRIORITY APPLICATION NUMBER: PCT/US00/05841
PRIORITY APPLICATION NUMBER: 60/232687          PRIORITY FILING DATE: 2000-03-02          PRIORITY APPLICATION NUMBER: PCT/US00/05841
PRIORITY FILING DATE: 2000-09-15          PRIORITY APPLICATION NUMBER: PCT/US00/06884
PRIORITY APPLICATION NUMBER: 60/180997          PRIORITY FILING DATE: 2000-03-15          PRIORITY APPLICATION NUMBER: PCT/US00/06884
PRIORITY FILING DATE: 1998-11-19          PRIORITY APPLICATION NUMBER: PCT/US00/08439
PRIORITY APPLICATION NUMBER: 09/218517          PRIORITY FILING DATE: 2000-03-30          PRIORITY APPLICATION NUMBER: PCT/US00/08439
PRIORITY FILING DATE: 1998-12-22          PRIORITY APPLICATION NUMBER: PCT/US00/13705
PRIORITY APPLICATION NUMBER: 09/284291          PRIORITY FILING DATE: 2000-05-17          PRIORITY APPLICATION NUMBER: PCT/US00/13705
PRIORITY FILING DATE: 1999-04-12          PRIORITY APPLICATION NUMBER: PCT/US00/14042
PRIORITY APPLICATION NUMBER: 09/380137          PRIORITY FILING DATE: 2000-05-22          PRIORITY APPLICATION NUMBER: PCT/US00/14042
PRIORITY FILING DATE: 1999-08-25          PRIORITY APPLICATION NUMBER: PCT/US00/14941
PRIORITY APPLICATION NUMBER: 09/380138          PRIORITY FILING DATE: 2000-05-30          PRIORITY APPLICATION NUMBER: PCT/US00/14941
PRIORITY FILING DATE: 1999-08-25          PRIORITY APPLICATION NUMBER: PCT/US00/15264
PRIORITY APPLICATION NUMBER: 09/380913          PRIORITY FILING DATE: 2000-06-02          PRIORITY APPLICATION NUMBER: PCT/US00/15264
PRIORITY FILING DATE: 1999-09-09          PRIORITY APPLICATION NUMBER: PCT/US00/22031
PRIORITY APPLICATION NUMBER: 09/403297          PRIORITY FILING DATE: 2000-08-11          PRIORITY APPLICATION NUMBER: PCT/US00/22031
PRIORITY FILING DATE: 1999-10-18          PRIORITY APPLICATION NUMBER: PCT/US00/23522
PRIORITY APPLICATION NUMBER: 09/423741          PRIORITY FILING DATE: 2000-08-23          PRIORITY APPLICATION NUMBER: PCT/US00/23522
PRIORITY FILING DATE: 1999-11-10          PRIORITY APPLICATION NUMBER: PCT/US00/30873
PRIORITY APPLICATION NUMBER: 09/4866034          PRIORITY FILING DATE: 2001-11-10          PRIORITY APPLICATION NUMBER: PCT/US00/30873
PRIORITY FILING DATE: 2001-05-25          PRIORITY APPLICATION NUMBER: PCT/US01/06666
PRIORITY APPLICATION NUMBER: 09/870238          PRIORITY FILING DATE: 2001-03-01          PRIORITY APPLICATION NUMBER: PCT/US01/06666
PRIORITY FILING DATE: 2001-11-08          PRIORITY APPLICATION NUMBER: PCT/US01/17092
PRIORITY APPLICATION NUMBER: 09/8020706          PRIORITY FILING DATE: 2001-12-01          PRIORITY APPLICATION NUMBER: PCT/US01/17092
PRIORITY FILING DATE: 2001-03-09          PRIORITY APPLICATION NUMBER: PCT/US01/17800
PRIORITY APPLICATION NUMBER: 09/918585          PRIORITY FILING DATE: 2001-02-28          PRIORITY APPLICATION NUMBER: PCT/US01/17800
PRIORITY FILING DATE: 2001-07-00          PRIORITY APPLICATION NUMBER: PCT/US01/19692
PRIORITY APPLICATION NUMBER: 09/924419          PRIORITY FILING DATE: 2001-06-20          PRIORITY APPLICATION NUMBER: PCT/US01/19692
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PRIORITY APPLICATION NUMBER: 09/927796          PRIORITY FILING DATE: 2001-06-29          PRIORITY APPLICATION NUMBER: PCT/US01/21066
PRIORITY FILING DATE: 2001-08-06          PRIORITY APPLICATION NUMBER: PCT/US01/21735
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PRIORITY FILING DATE: 2001-08-13          PRIORITY APPLICATION NUMBER: PCT/US01/27099
PRIORITY APPLICATION NUMBER: 09/941992          PRIORITY FILING DATE: 2001-08-29          PRIORITY APPLICATION NUMBER: PCT/US01/27099
PRIORITY APPLICATION NUMBER: 09/946374          NUMBER OF SEQ ID NOS: 91
PRIORITY APPLICATION NUMBER: PCT/US99/00106          SEQ ID NO: 24
PRIORITY APPLICATION NUMBER: PCT/US98/18824          LENGTH: 567
PRIORITY APPLICATION NUMBER: PCT/US98/18824          TYPE: PRT
PRIORITY APPLICATION NUMBER: PCT/US98/18824          ORGANISM: Homo Sapien
US-10-001-054-24

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Query Match Score 999; DB 13; Length 567;  
 Best Local Similarity 41.8%; Pred. No. 2.8e-74; Mismatches 99; Indels 32; Gaps 9;  
 Matches 217; Conservative

Qy 3 LHVVKWKSUVSVLTVYHT-VALSISKEHLACDLCBHDYTLQTLQTLNGLPHINTSHH 61  
 Db 6 LH---LVLPVILSLIASQDWKAERSQDPFPEKCMQDPYEQULLKVTVGLNRTLKQR 61

Qy 62 WIVGAGAGLTAALKJJDAGHTVTILEANDRIGGRVETYNEKEGHYAEMGAMRTPSH 121  
 Db 62 VIVGAGAGLVAALKVLDAGHKVTLADNRIGGRITTYRDONTGHJELGAMRMSSH 121

Qy 122 RIVQWFVKLGVMENMFMTDDNTFYLNGVRERTYVQENPDVLKVNVSSEKGTSADD 181  
 Db 122 RILHKLCCQGLGLNLTKFQYDKNNTWTEYHEVKLRNYYTEKVPEKLGALRQPDKHSPEED 181

Qy 182 LLDRALQKVKEEVBANGRAALEKDYDRVSKEYLKEEGLSPGAVRMGLINEQSIMYT 241  
 Db 182 IYQMALNQALKDLKALGCRKAMKKPERHTLLEULLGEGLNSRPAVQLGDVNSEDGPFYI 241

Qy 242 AUSEMIVQADYNDSDVTTHEVTCGSDLIPEAFLSVLDPILLNSKVKHTRQSDKGTVSY 301  
 Db 242 SFABALRHSCLDRQSRIVGWDLPRALSSLSSGLVLAAPVAMTQSPHDYHVIQI 301

Qy 302 QTGNES-SLMDS-SADIIVLVTTAKAALFDPPLSISKMEALRSVYDSTSSTKILLTFRD 360  
 Db 302 ETCPPARNLKVLKADWVILTASCPAVKRITFSPLPRLPHMOELRRHYVPATKVELSRR 361

Qy 361 KFWDDDGIRGGKSITDGPSRYIYPHSFHNTNETIGVLLASYTWSDESLFLGASDEBLK 420  
 Db 362 PFWREHIEGGHSNTDRPSRMIFYP---PPREGALLASYTWSDAAAFPGLSREAL 416

Qy 421 EALRDIAKIHG--EQWWDKCTGVYTKWMSADPSUGAFALFTPIQHLEAQUELSS-E- 476  
 Db 417 RLALDDYALHGVRQWLDG-TGV-YKRWADQHSGOFVQQPP-----ALMOTEK 466

Qy 477 -----GRVHFAGENTPAPHANIETSMKSARAATMIN 508  
 Db 467 DDMTVPGRYFAGEHTAYPHGMVETAWKSALARATKIN 505

**RESULT 8**  
 US-10-053-107-2  
 / Sequence 2, Application US/10053107  
 / Publication No. US2020201922752B1  
 / GENERAL INFORMATION  
 / APPLICANT: Goddard, Audrey  
 / APPLICANT: Godowski, Paul J.  
 / APPLICANT: Gurney, Austin L.  
 / APPLICANT: Hillan, Kenneth J.  
 / APPLICANT: Tumas, Daniel  
 / APPLICANT: Watanahe, Colin K.  
 / APPLICANT: Wood, William I.  
 / TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune  
 / FILE REFERENCE: P3033RC1  
 / CURRENT APPLICATION NUMBER: US/10/053.107  
 / CURRENT FILING DATE: 2002-01-17  
 / PRIOR APPLICATION NUMBER: 60/108802  
 / PRIOR FILING DATE: 1998-11-17  
 / PRIOR APPLICATION NUMBER: 60/113296  
 / PRIOR FILING DATE: 1998-12-22  
 / PRIOR APPLICATION NUMBER: 60/131291  
 / PRIOR FILING DATE: 1999-04-27  
 / PRIOR APPLICATION NUMBER: 60/151733  
 / PRIOR FILING DATE: 1999-08-31  
 / PRIOR APPLICATION NUMBER: 60/209832  
 / PRIOR FILING DATE: 2000-06-05

/ PRIOR APPLICATION NUMBER: 60/232887  
 / PRIOR FILING DATE: 2000-09-15  
 / PRIOR APPLICATION NUMBER: 09/218517  
 / PRIOR FILING DATE: 1998-12-22  
 / PRIOR APPLICATION NUMBER: PCT/US99/00106  
 / PRIOR FILING DATE: 1999-01-05  
 / PRIOR APPLICATION NUMBER: PCT/US99/20111  
 / PRIOR APPLICATION NUMBER: PCT/US99-01-01  
 / PRIOR FILING DATE: 2000-05-17  
 / PRIOR APPLICATION NUMBER: PCT/US00/04342  
 / PRIOR FILING DATE: 2000-02-18  
 / PRIOR APPLICATION NUMBER: PCT/US00/05501  
 / PRIOR FILING DATE: 2000-03-01  
 / PRIOR APPLICATION NUMBER: PCT/US00/13705  
 / PRIOR FILING DATE: 2000-05-17  
 / PRIOR APPLICATION NUMBER: PCT/US00/14042  
 / PRIOR FILING DATE: 2000-05-22  
 / PRIOR APPLICATION NUMBER: PCT/US00/14941  
 / PRIOR FILING DATE: 2000-05-30  
 / PRIOR APPLICATION NUMBER: PCT/US00/15264  
 / PRIOR FILING DATE: 2000-06-02  
 / PRIOR APPLICATION NUMBER: PCT/US00/23522  
 / PRIOR FILING DATE: 2000-08-23  
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 / PRIOR FILING DATE: 2000-08-24  
 / PRIOR APPLICATION NUMBER: PCT/US00/32678  
 / PRIOR FILING DATE: 2000-12-01  
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 / PRIOR FILING DATE: 2001-06-01  
 / PRIOR APPLICATION NUMBER: PCT/US01/19692  
 / PRIOR FILING DATE: 2001-06-20  
 / PRIOR APPLICATION NUMBER: PCT/US01/21066  
 / PRIOR FILING DATE: 2001-06-29  
 / PRIOR APPLICATION NUMBER: PCT/US01/21735  
 / PRIOR FILING DATE: 2001-07-09  
 / NUMBER OF SEQ ID NOS: 14  
 / SEQ ID NO 2  
 / LENGTH: 567  
 / TYPE: PRT  
 / ORGANISM: Homo Sapien  
 / US-10-053-107-2

Query Match Score 999; DB 13; Length 567;  
 Best Local Similarity 41.8%; Pred. No. 2.8e-74; Mismatches 99; Indels 32; Gaps 9;  
 Matches 217; Conservative

Qy 3 LHVVKWKLSSVSVLTVYHT-VALSISKEHLACDLCBHDYTLQTLQTLNGLPHINTSHH 61  
 Db 6 LHL---LVLPVILSLIASQDWKAERSQDPFPEKCMQDPYEQULLKVTVGLNRTLKQR 61

Qy 62 VIVGAGAGLTAALKJJDAGHTVTILEANDRIGGRVETYNEKEGHYAEMGAMRTPSH 121  
 Db 62 VIVGAGAGLVAALKVLDAGHKVTLADNRIGGRITTYRDONTGHJELGAMRMSSH 121

Qy 122 RIVQWFVKLGVMENMFMTDDNTFYLNGVRERTYVQENPDVLKVNVSSEKGTSADD 181  
 Db 122 RILHKLCCQGLGLNLTKFQYDKNNTWTEYHEVKLRNYYTEKVPEKLGALRQPDKHSPEED 181

Qy 182 LLDRALQKVKEEVBANGRAALEKDYDRVSKEYLKEEGLSPGAVRMGLINEQSIMYT 241  
 Db 182 IYQMALNQALKDLKALGCRKAMKKPERHTLLEULLGEGLNSRPAVQLGDVNSEDGPFYI 241

Qy 242 AUSEMIVQADYNDSDVTTHEVTCGSDLIPEAFLSVLDPILLNSKVKHTRQSDKGTVSY 301  
 Db 242 SFABALRHSCLDRQSRIVGWDLPRALSSLSSGLVLAAPVAMTQSPHDYHVIQI 301

Qy 302 QTGNES-SLMDS-SADIIVLVTTAKAALFDPPLSISKMEALRSVYDSTSSTKILLTFRD 360  
 Db 302 ETCPPARNLKVLKADWVILTASCPAVKRITFSPLPRLPHMOELRRHYVPATKVELSRR 361

Qy 361 KFWDDDGIRGGKSITDGPSRYIYPHSFHNTNETIGVLLASYTWSDESLFLGASDEBLK 420  
 Db 362 PFWREHIEGGHSNTDRPSRMIFYP---PPREGALLASYTWSDAAAFPGLSREAL 416

Qy 421 EALRDIAKIHG--EQWWDKCTGVYTKWMSADPSUGAFALFTPIQHLEAQUELSS-E- 476  
 Db 417 RLALDDYALHGVRQWLDG-TGV-YKRWADQHSGOFVQQPP-----ALMOTEK 466

Qy 477 -----GRVHFAGENTPAPHANIETSMKSARAATMIN 508  
 Db 467 DDMTVPGRYFAGEHTAYPHGMVETAWKSALARATKIN 505

Qy 421 ELALRDLAKING---EQWWDKCTGIVVKKMSADPYSLGGAFALFTPYQHLEYAQUELFSSE- 476  
 Db 417 RQLDDYDHALGPVVRQWLDG-TGV-YKRWAQDOHSQGFVQPP-----ALWOTEK 466

Qy 477 -----GRVHFAGEHTAPPHAWIETSMKSATRAATNIN 508  
 Db 467 DDKTVPICRIVFGEHTAPPHGMVETAKSALRAAIKN 505

---

RESULT 9

US-10-028-072-476

Sequence 476, Application US/10028072

Publication No. US2003004311A1

GENERAL INFORMATION

APPLICANT: Baker, Kevin P.  
 APPLICANT: Beresini, Maureen  
 APPLICANT: DeForge, Laura  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerritson, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Sherwood, Steven  
 APPLICANT: Smith, Victoria  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K  
 APPLICANT: Wood, William  
 APPLICANT: Zhang, Zheng

TITLE OF INVENTION:  
 FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/028.072

CURRENT FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/049911

PRIOR FILING DATE: 1997-06-18

PRIOR APPLICATION NUMBER: 60/056974

PRIOR FILING DATE: 1997-08-26

PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059115

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PRIOR FILING DATE: 1997-09-24

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/062285

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 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090429  
 PRIOR APPLICATION NUMBER: 60/090445  
 PRIOR APPLICATION NUMBER: 60/090538  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR FILING DATE: 1998-07-07

Qy 62 VVIVGAGMAGLTAAKLLDAGHTVTILEANDRGRVETYRNKEGVWAEAGMARISSH 121  
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 Qy 122 RIVQWFYRKLGIVEMNEFVMTDDNTFYLVNGVRERTYYVQENPDVLKVNVSESEKGISADD 181  
 Db 122 RILHKLCOGSLGLNLTKETQDKNNTWEVEVKLNNTVEKPEKGALRPQEKGHSPEED 181  
 Qy 182 LLDRALOKVKVEEYANGCKAALEKYDKEYSYKEVYLKEGGISPGAVRMIGDLUNEQSLUMT 241  
 Db 182 IYQMLNQALDKLQALKCRAKMKFEHTLLEYLGEGLNSRPAVQJGDMNSEDFGFYL 241  
 Qy 242 ALSEMIDQADVNDSVTYHEVIGSDILPEAFLSVDPLILNSKVKHIRDQDKGVIVSY 301  
 Db 242 SPAELRAHSCLSLDQLQYSRTVGGWDLPLRAILSLSGLVLLNAPVVAMTQGPHDYRVQI 301  
 Qy 302 QPGNES-SLMDSLADIVLVTTAKAALFDIDPPLSISMEALSRYHDSSSTKILLTFRD 360  
 Db 302 ETSPPARNLKVLKDVVLTASGPVKRITSPPPLRHMQEALRLHYVPATKVLFLSFR 361  
 Qy 361 KEWEDDGIRGGGSTIDGPSRTVYKWKSAAPDYSUAGAFLPTYOHLEYAQELFSSS- 476  
 Db 362 PFWREHIEGGNSNTDRSPRMIFYP-----PERGAGLLASTWSDAAAFAGLSREBAL 416  
 Qy 421 ELALRDIAKING--EQWWDKCTGVYKWKSAAPDYSUAGAFLPTYOHLEYAQELFSSS- 476  
 Db 417 RLALDDVAALHCPVVRQLWDG-TGV-WKRWAEDQHSQCGFVYQPP-----ALWQTEK 466  
 Qy 477 -----GRVHPAGEATAFHAWETSMSKAIRATAATMIN 508  
 Db 467 DDTWTPVGRYIYFAGEHTAYPHGWETAVKSALARAIKIN 505

RESULT 10  
 US-10-14-808-476  
 Sequence 476, Application US/10140808  
 ; Publication No. US20030017563A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Beresini, Maureen  
 ; APPLICANT: DeForge, Laura  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Filvaroff, Allen  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Sherwood, Steven  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watabane, Colin K  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEARIC  
 ; ACIDS ENCODING THE SAME  
 ; FILE REFERENCE: P3330R1C182  
 ; CURRENT APPLICATION NUMBER: US/10/140,808  
 ; CURRENT FILING DATE: 2002-05-07  
 ; Prior Application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 550  
 ; SEQ ID NO 476  
 ; LENGTH: 567  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 ;  
 Query Match 37.0%; Score 999; DB 14; Length 567;  
 Best Local Similarity 41.8%; Pred. No. 2.8e-74; Length 567;  
 Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;  
 Qy 3 LHVVKKLSSVSVLITYSHT-VALSLSKEHLADCLEDKDYLQTLQDNLPHINTSHH 61  
 Db 6 LH-----LVLVPLILLSIVASQDWKAERSQDPPEKCMQDPDYEQLLCWTWGLNRTLKPKQR 61

Qy 3 LHVKWKLSVSVVSLITLXSYHT-VALSLKEHLADCLEDKDYDTLLQTLNLPHNTSHH 61  
 Db 6 LHL---LVLPILLSLVAQSKWKAERSQDPPEKCMQDPEQLLKVTNLRKPR 61  
 Qy 62 VVIVGAGAGLTAALKLQDAQHTVTILEANDRUGGRVETYNEKEGYAEMGAMRIPSSH 121  
 Db 62 VVIVGAGAGLVAALKLQDAQHTVTILEADNRIGGRFTYDQNTGWIGEJGMAMPSSH 121  
 Qy 122 RIVQWFVKKLGVEMIEFMTDNTFLYNGPERTYVQENPDVLKYNVSESEKGISADD 181  
 Db 122 RTLKLUCCGLGNLTKEQDQNTWTWVEYLRLNVKEPEKLGAYLREQEKHSPEQD 181  
 Qy 182 LDRLALOKVKEVEANGCAALEKYDYSVKEYLKEBGLSPGAVMIGDLNLNEOSLMYT 241  
 Db 182 IQMANALQKALKLAKSGRKAMKKFEEFHLLFEGNSRSPAVOLGDYMSEDDFYI 241  
 Qy 242 ALSEMITYDQADYNDTSVYTHEVTTGSDULPEAFSLVDPLILNSKTKHROSDFKVTVSY 301  
 Db 242 SFAEALRAHSCLSDRQLQSRIVGWDLIPRALLSSGLVLLNAPVATMOPGHDVHQI 301  
 Qy 302 QGNES-SLMDSLSDADVLTAAKALFIDFPPLSISKMPALRSVHDSSSTKILLTFRD 360  
 Db 302 ETSPPARNLKVKRADVVLTLTASGPVKRITFSPPLRHMQEARLRRHYPATKVFUSFR 361  
 Qy 361 KFWDDDGIRGCKSITDGPSSRYIYPHSFSHTNETIGVLASYTWSDSLLFIGASDEELK 420  
 Db 362 PFWREEHTEGGHSNTDPSRMFYP----PPREGAILLASTWSDAAAFAGLREEA 416  
 Qy 421 EIALRDLAKING---EOWWDKCTGTIVKQWKSADPYSIQLGAFALFPTVQHLEYAQELFSS-E 476  
 Db 417 RLALDDPAALHGPPVVRQLWDG-TGV-VKRWADQHSGQGFVQQP-----ALWOTEK 466  
 Qy 477 -----GRVHPAGEHTAAPHWAIETSMKSAIRATTNIN 508  
 Db 467 DDWTVPyGRYIYPAGEHTAIPHGWETAVSKSALRAAIKIN 505

RESULT 11  
 US-10-121-049-476  
 Sequence 476, Application US/10121049  
 Publication No. US200300223941  
 GENERAL INFORMATION:  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Beresini, Maureen  
 APPLICANT: Desorge, Laaura  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Sherwood, Steven  
 APPLICANT: Smith, Victoria A.  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K  
 APPLICANT: Wood, William  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME  
 FILE REFERENCE: P3330R1C17  
 CURRENT APPLICATION NUMBER: US/10/121,049  
 CURRENT FILING DATE: 2002-04-12  
 Prior Application removed - See File Wrapper or Palm  
 NUMBER OF SEQ ID NOS: 550  
 SEQ ID NO 476  
 LENGTH: 567  
 TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 US-10-121-049-476  
 Query Match 37.0%; Score 999; DB 14; Length 567;

Best Local Similarity 41.8%; Pred. No. 2.8e-74;  
 Matches 217; Conservative 99; Mismatches 171; Index 32; Gaps 9;

Qy 3 LHVKWKLSVSVVSLITLXSYHT-VALSLKEHLADCLEDKDYDTLLQTLNLPHNTSHH 61  
 Db 6 LHL---LVLPILLSLVAQSKWKAERSQDPPEKCMQDPEQLLKVTNLRKPR 61  
 Qy 62 VVIVGAGAGLTAALKLQDAQHTVTILEANDRUGGRVETYNEKEGYAEMGAMRIPSSH 121  
 Db 62 VVIVGAGAGLVAALKLQDAQHTVTILEADNRIGGRFTYDQNTGWIGEJGMAMPSSH 121  
 Qy 122 RIVQWFVKKLGVEMIEFMTDNTFLYNGPERTYVQENPDVLKYNVSESEKGISADD 181  
 Db 122 RTLKLUCCGLGNLTKEQDQNTWTWVEYLRLNVKEPEKLGAYLREQEKHSPEQD 181  
 Qy 182 LDRLALOKVKEVEANGCAALEKYDYSVKEYLKEBGLSPGAVMIGDLNLNEOSLMYT 241  
 Db 182 IQMANALQKALKLAKSGRKAMKKFEEFHLLFEGNSRSPAVOLGDYMSEDDFYI 241  
 Qy 242 ALSEMITYDQADYNDTSVYTHEVTTGSDULPEAFSLVDPLILNSKTKHROSDFKVTVSY 301  
 Db 242 SFAEALRAHSCLSDRQLQSRIVGWDLIPRALLSSGLVLLNAPVATMOPGHDVHQI 301  
 Qy 302 QGNES-SLMDSLSDADVLTAAKALFIDFPPLSISKMPALRSVHDSSSTKILLTFRD 360  
 Db 302 ETSPPARNLKVKRADVVLTLTASGPVKRITFSPPLRHMQEARLRRHYPATKVFUSFR 361  
 Qy 361 KFWDDDGIRGCKSITDGPSSRYIYPHSFSHTNETIGVLASYTWSDSLLFIGASDEELK 420  
 Db 362 PFWREEHTEGGHSNTDPSRMFYP----PPREGAILLASTWSDAAAFAGLREEA 416  
 Qy 421 EIALRDLAKING---EOWWDKCTGTIVKQWKSADPYSIQLGAFALFPTVQHLEYAQELFSS-E 476  
 Db 417 RLALDDPAALHGPPVVRQLWDG-TGV-VKRWADQHSGQGFVQQP-----ALWOTEK 466  
 Qy 477 -----GRVHPAGEHTAAPHWAIETSMKSAIRATTNIN 508  
 Db 467 DDWTVPyGRYIYPAGEHTAIPHGWETAVSKSALRAAIKIN 505

RESULT 12  
 US-10-123-204-476  
 Sequence 476, Application US/10123904  
 Publication No. US20030022328A1  
 GENERAL INFORMATION:  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Beresini, Maureen  
 APPLICANT: Desorge, Laaura  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Sherwood, Steven  
 APPLICANT: Smith, Victoria A.  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K  
 APPLICANT: Wood, William  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME  
 FILE REFERENCE: P3330R1C54  
 CURRENT APPLICATION NUMBER: US/10/123,904  
 CURRENT FILING DATE: 2002-04-16  
 Prior Application removed - See File Wrapper or Palm  
 NUMBER OF SEQ ID NOS: 550  
 SEQ ID NO 476  
 LENGTH: 567  
 TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 US-10-121-049-476  
 Query Match 37.0%; Score 999; DB 14; Length 567;

US-10-123-904-476

Query Match 37.0%; Score 999; DB 14; Length 567;

Best Local Similarity 41.8%; Pred. No. 2, 8e-74;

Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

Length: 567

TYPE: PRT

ORGANISM: Homo Sapien

US-10-140-470-476

Query Match 37.0%; Score 999; DB 14; Length 567;  
 Best Local Similarity 41.8%; Pred. No. 2, 8e-74;  
 Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

Qy 3 LHVVKWLSVSVLILYHTSHT-VALSKEHLADCLPDKDYLTLQTDNLGPHINTSHH 61  
 Db 6 LHL----LVLPIPLSLVASQDWKAERQDPFECRMDQDPYBOLLKVTWGNRTRKPCR 61

Qy 62 VVVGAGHAGLTAKLLODAGHTTILEANDRIGRFLTYRQNTGIGLGMARMPSSH 121  
 Db 62 VVVGAGHAGLTAKLLODAGHTTILEANDRIGRFLTYRQNTGIGLGMARMPSSH 121

Qy 122 RIVQWFVKKLGVERMNEFTMDNTFLYNGVRERTYQQENPDVLKYNVSESEKGISADD 181  
 Db 122 RILHKLCQGLGLNLTKFQYDQTKNTWTEHEVKLRNYVEKVPEKLYALRQEKGHSPE 181

Qy 182 LIDRALQKVEEYANGCKAALEKYDVRYSKEVLRKGGLSPGAVRMIGDLIENEOLMYT 241  
 Db 182 RILHKLCQGLGLNLTKEFDQTKNTWTEHEVKLRNYVEKVPEKLYALRQEKGHSPE 181

Qy 242 ALSEMIVYQADYNSVTYHEVTTGSDLLPEAFISLVDILLPKVLSLQVYAMTQGPHDYHVI 301  
 Db 242 SPAEALRAHSCLSDRLOYSRITVGGWDULPRAUSSLSSGLVLIINAPVYAMTQGPHDYHVI 301

Qy 302 QTNQES-SLMDSLADIVVTTATAAALFIDFOPPLTSKMEALRSYHDSSTKILLTFRD 360  
 Db 302 ETSPPARNLKVKAADVLLTASPAVKRITFSPPLRPHMQLEARRLHYVPAKVFSLRR 361

Qy 361 KFWDDGIRGGKSITDGFPSRYIYPPSHSFHTNETIGVIALASTWSDESLLFGLGASDEBK 420  
 Db 362 PFWREEHTEGGSNTDRESMTFYP----PEREGALLLASTWSDAAAAGLSSBEAL 416

Qy 421 EALRLDLAKHG--EQWWDKCTGTIVKVKWKSADPSLGAFAFLPTYQHLEYAQELFSE- 476  
 Db 417 RLALDDVAALHGPVVRQWLWDG-TGV-VKRAWEQDQHSQGFVQQP-----ALWQTEK 466

Qy 477 -----GRVHFAGENTAFAHWIETMSKSAIRATAATNN 508  
 Db 467 DDWTVPYGRIVFAGENTAPYHGMVETAWSALRAAIKN 505

RESULT 13  
US-10-140-470-476Publication No. US20030022331A1  
GENERAL INFORMATION

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: DeForge, Laura

APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William

APPLICANT: Zheng, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P1330R1C160

CURRENT FILING DATE: 2002-05-06

Prior Application removed - See Palm or File Wrapper

NUMBER OF SEQ ID NOS: 550

SEQ ID NO 476

RESULT 14  
US-10-175-746-476

Sequence 476, Application US/10175746

Publication No. US2003002270A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: DeForge, Laura

APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William

APPLICANT: Zheng, Zemin

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3330R1C353

CURRENT APPLICATION NUMBER: US/10/175,746

CURRENT FILING DATE: 2002-06-19

Prior Application removed - See File Wrapper or Palm  
 NUMBER OF SEQ ID NOS: 550  
 SEQ ID NO 47  
 LENGTH: 567  
 TYPE: PRT  
 ORGANISM: Homo Sapien  
 US-10-175-746-476

Query Match	37.0%	Score 999; DB 14; Length 41.8%; Pred. No. 2.e-74;
Best Local Similarity	41.8%	Mismatches 171; I
Matches 217; Conservative		
3 LHVVKWKLSSVVLITLYSHT VAIISLKEHADCLEDKYD		
6 LHL ---LVLPVLLSVAQOMKAERSODPPEKQMDPDIYE		
62 VIVIGAGMAGLTAAKLLODAGHVVTEIANDEVGRVETARN		
62 VIVIGAGVAGLVAAKVLSDAAGHKVTEIADNFIGGIFTYRD		
122 RIVQWMFVKLGVMENNEFWYMTDNTFYLVNGYERBERTTYVQENP		
62 VIVIGAGVAGLVAAKVLSDAAGHKVTEIADNFIGGIFTYRD		
122 RILHKLQCQGLNLTKFTQYDQNTWTVEHEVFLRNYYVEKUP		
182 LDDEALQKVKEYEAVANGKAALPDKYDVSXKYLKEEGGJSP		
182 LYQNALNQALDKLALGERKMKFERTHLLEVLGEGNLSR		
242 ALSEMIDQADVNDSVTYHEVTGGSDLILPEAFLSVLDVPILL		
242 SFAEARLHSCLSDRLQYSRIVGWDLIPRALISSLGLVLI		
302 QTGNES-SLMNLDASDIVLVTTAKAALPFDPPPLSKMPE		
302 ETSPPARNLKVLAKDVLVLTASGPRAVKRITFSPPLPRHMQB		
361 KFWEDDGIORGKSITDGPERYTPVPSHSHTNTIGVLLAS		
362 FFWREEHIEBGHSNTDRPRSMIFPP---PREGALLIAS		
421 BLAIRDLAKHG---EQWNDKCTGIVVICKWSADPYSLGAFAN		
417 RJALDDVVAIHPVVRQLND-TGV - VRKWTDOHSQGFTV		
477 -----GRVHFAGEHTTAAPHAWIETSMKSAIRAAATIN 5C		
467 DDWTVBYGRIFTYFAGEHTAYPHGWVETAVSALARAAIKIN 5C		

RESULT 15 US-10-176-918-476  
 ; Sequence 476, Application US/10176918  
 ; Publication No. US20030027275A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Beresini, Maureen  
 ; APPLICANT: DeForge, Laura  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Sherwood, Steven  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K  
 ; APPLICANT: Wood, William  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES ENCODING THE SAME

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; FILE REFERENCE: F3330R1C382
; CURRENT APPLICATION NUMBER: US/10/176,918
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO: 476
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo Sapien
; SEQ-ID-NR: US-10-176-918-476

Query Match, Score 999, DB 14; Length 567;
Best Local Similarity 41.8%; Pred. No. 2.8e-14;
Matches 217; Conservative 99; Mismatches 171; Indels 32; Gaps 9;

Qy 3 LHVVKRKLSSVSLITLYYSHT-VALSLKEHLADLCEDKDYDTLCLQLDNLGHPLHINTSHH 61
Db 6 LHL---LVLQVAVASODWKARSQDPPEKCNQDPDVQLLKVVTWGLNRTLKPOR 61

Qy 62 VVIVGAGMAGLTAAKLQDAGHTVTLLEANDRGGVETYNEKEGMYAENGAMRLPSSH 121
Db 62 VVIVGAGVAGLVAAKVLSDAGHKVTLLEADNRIGGRFLTYRQNTGWIGELGAMRMPSHH 121

Qy 122 RIVQWFFYRKLGIVEMNFVMTDNTTFYLVNGVRERTYQQENPDVLYKVNVESEKGISADD 181
Db 122 RLHKLCGQGLGNLTKEQDNTTWEVHEVLRNNTVEKPFKLGYALRPQEKGHSPEED 181

Qy 182 LLDRALQVKVEANGKAALKYDRYSVKELFEGGLSPGAVRMIGDLNEQSILMVT 241
Db 182 TYOMALNQALKDIALGKRKMKFERTHLLEYLGBNSLSRAVQLQGDVNSEDGFYI 241

Qy 242 ALSEMIVYDQADNDSTVYHEVTCGSQDLPEARLSSVLDVPIILNSKVKHIIROSDPKGVIVSY 301
Db 242 SFEEALAHSCSLDRQYSRIVGMDLPRALISSSGSLVLLNAPPVAMTQGPBHDVHQI 301

Qy 302 OTGNES-SLMDSIADVLTAKAALFTDFDPLLSKMEALRSVHYDSSSKILLTPRD 360
Db 302 ETSPPARNLKVKAADVLLTAGPAVRIKTTFSPLPRHMQEALRRLHYVPATKVLSPRR 361

Qy 361 KEWDGIRGKKSITDGPSRYIYPHSFHNTNETIGVILASTWSDESLFLGASDEEKK 420
Db 362 PEFRVHEHEGGHNTDRSRM FYP-----PPREGALLASTWSDAAAFAGLSREEAAL 416

Qy 421 ELLARDLAKHG--EQWIDKCTGVYVKWSSADPYSLGAFALFTPYQHLEYAQBLFESSP- 476
Db 417 RLALDDVAALHGPPVROLWDG-TGV--VGRWAEDQHSSQGFWOP-----ALWQTEK 466

Qy 477 -----GRVHFPAGETTAHPHAWIETMSKSAIAATTNN 508
Db 467 DDWTVPYGRIFAGEHTAYPHGWVETAVSKALRAAIKIN 505

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OM protein - protein search, using SW model

Run on: October 4, 2005, 13:48:15 ; Search time 43 Seconds  
(without alignments)

1172.502 Million cell updates/sec

Title: US-10-645-094-1

Perfect score: 2703

Sequence: 1 MNLHVVKLSSLVSLITX.....TNINKVANEESTIHTKDEL 524

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: Pir1:\*

2: Pir2:\*

3: Pir3:\*

4: Pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105.5	39.2	516	JB0266	L-amino-acid oxida
2	105.5	39.0	516	JC8015	L-amino-acid oxida
3	73.5	27.3	446	B69999	L-amino acid oxida
4	64.1	23.7	701	JC8062	L-glutamate oxidas
5	41.2	15.2	526	A75581	flavin monooxidase
6	39.2	14.5	426	A12498	L-amino acid oxida
7	39.2	14.5	695	A38314	L-amino-acid oxida
8	38.5	14.2	541	A87595	amine oxidase, fla
9	35.5	13.1	534	G87384	amine oxidase, fla
10	30.7	11.4	496	H83592	hypothetical prote
11	30.2	11.2	557	A25493	tryptophan 2-monoo
12	28.8	10.7	520	JH0417	amine oxidase (fla
13	28.5	10.6	723	S30105	tryptophan 2-monoo
14	28.5	10.6	500	T03387	polyamine oxidase
15	28.3	10.5	527	A61715	amine oxidase (fla
16	28.3	10.5	556	A53376	tryptophan 2-monoo
17	27.1	10.0	520	A31870	amine oxidase (fla
18	27.0	10.0	526	JT0528	amine oxidase (fla
19	26.9	10.0	471	S72920	hypothetical prote
20	26.7	9.9	1265	F71429	tryptophan 2-monoo
21	26.5	9.8	755	A11228	tryptophan 2-monoo
22	25.9	9.6	755	DAAGWT	amine oxidase (fla
23	25.6	9.5	499	I51346	hypothetical prote
24	25.5	9.3	527	S30374	tryptophan 2-monoo
25	25.1	9.3	755	Q0A64T	amine oxidase (fla
26	24.8	9.2	803	T24685	hypothetical prote
27	24.5	9.0	448	H70947	hypothetical prote
28	24.5	9.0	478	A41693	putrescine oxidase
29	24.2	9.0	516	D96682	protein F1B22.18 [

## ALIGNMENTS

RESULT 1  
JE0266  
L-amino-acid oxidase (EC 1.4.3.2) - eastern diamondback rattlesnake  
N;Alternate name: LAAO; ophio-amino-acid oxidase  
C;Species: Crotalus adamanteus (eastern diamondback rattlesnake)  
C;Date: 05-Feb-1999 #sequence revision 05-Feb-1999 #text change 09-Jul-2004  
C;Accession: JE0266  
R;Raibekas, A.A.; Massey, V.  
Biochem. Biophys. Res. Commun. 248, 476-478, 1998  
A;Title: Primary structure of the snake venom L-amino acid oxidase shows high homology .  
A;Reference number: JB0266; MUID: 98169573; PMID: 9703950  
A;Accession: JE0266  
A;Molecule type: mRNA  
A;Cross-references: <RAI>  
A;Residues: 1-516 <RAI>  
C;Keywords: oxidoreductase

Query Match 39.2%; Score 1059.5; DB 2; Length 516;  
Best Local Similarity 44.0%; Pred. No. 1.1e-00;  
Matches 218; Conservative 94; Mismatches 171; Indels 13; Gaps 7;

Qy 33 LADCLDEDKDYYDTLLOTIDLNGLPHINTSHVYVTVGAGMAGLTAAKLJJDAGHTVTILBAND 92  
Db 25 LEBCFRTDYBESFLAKNGLTATNSPKRVVAGAGLSSRAYVLAGAGHOVTEASE 84

Qy 93 RVGGVETYNEKEGTYAEMGAMRIPSHRYQWPFVKKGYEMNFVMTDDNTFYLYNGV 152  
Db 85 RVGGRVFTYR-KDQNYANLGPMLRTKHRIVREYIKKFDLKLNEFSEQENENAWYFKNI 142

Qy 153 RERTYYQENPDVLYKTVNVESEKGKISADDLDRALQRKVKEEANGCKAALEKYDRYSVK 212  
Db 143 RKRVREVKNPOLLPEPVKPSBEGGSAQAQLYVESLRKVBELRSNCKVILDKYDYSTK 202

Qy 213 EYLKEGGLSPGAVRMGDLINNEQSLMTALSEMIMYDQADYNDSVITYHEVTGGSDLPPEA 272  
Db 203 EYLKEGGLSPRAVDNTGDLINNEQSLYVSPTESLRHDDIGYEKRFDETVGMDDQPS 262

Qy 273 FLSVL--DVPILLNSKVKHROSDKGIVVSYQT-GNESSLMDSLADIVLVTTAKALFI 329  
Db 263 MYEAIKEKVQVHFNAVRVIEQONDREATVYQTSAIEMS--SVTADEVCTTSRAARRI 320

Qy 330 DFDPLPLISKMEARLSVHYDSTSLLTFRKFWEDDGIRGSGKSITDGPSRYIYYPSHSF 389

Qy 390 HTNETIGVLLASYTWSDESLFLFGASDEELKELAIDLAKTH--GEQWWDKCTGVIVKK 446

Db 321 KFEPPLPKKAHALRSVHYRSGTKIPICTKFKFWEDDGIHGGSSTTDLPSRFIYWPNNF 380

Qy 381 TSG--YGVIA-YGICBDANFQQLDFKDCADIVNDLSLHELPKEDIDQFCPSKNIQ 437

Qy 447 WSADPYSLGAFALPTPYQHLEYAQLEFSSEGRVHAGEHTAAPHAMIEETSMSKAIRATN 506

Db 438 WSLDKYAMGGGITTPYQFHSEALTAPKRIYFAGEYTAOFQHGWIDSTIKSGLTAARD 497



A;Reference number: JC8062; PMID: 14769868

A;Accession: JC8062

A;Molecule type: DNA

A;Residues: 1-701 &lt;ARR&gt;

A;Cross-references: DDBJ:AB085623

A;Experimental source: (Strain X-119-6)

C;Comment: This enzyme precursor is a protein of 150k with hexamer structure alpha2-beta2 non-covalently bound PAD as a cofactor. It catalyzes the oxidative deamination of an L-glutamate existing in food and in a fermentation process.

C;Genetics:

A;Gene: Lgox

A;Start Codon: GTG

C;Keywords: hexamer structure; L-glutamate oxidase

Query Match 23.7%; Score 641; DB 2; Length 701;

Best Local Similarity 27.2%; Pred. No. 1.8e-33;

Matches 95; Mismatches 195; Indels 164; Gaps 14;

Qy 49 LONGLPHINTSHHIVVAGAGLTAAXLLQDAGHTVTILEAN-DRGGRVETYRNEK-- 105

Db 48 IDGLNPQGPKRILIVAGIQLVAGULTRAGHDVTILEANANRGRITFKHAKGE 107

Qy 106 -----EGWAEMGAMRIPSSHRIQWVTFKLGVEENNFFVMTDDN-----TFY 147

Db 108 PSPFADPAQYAEGAMRILPSFHPTLALIDKGKLKRIFENVDIDPOTGNQDAPVPPFY 167

Qy 148 -----LVNGV-----RETYVQENPDVLK-----XNVSESEKG 176

Db 168 KSFKDGTWTWNGAPSPEEPEPKDKRNTHTWIRTNREQRRAQYATDPSSINEFPHLTGCTR 227

Qy 177 ISADDLIDPRLDKRYKEEVEAN-----GCKAALEKDYRSVKEYLKEGG 220

Db 228 LTVDMDVNQALEFVRDYYTSVKQDDGTRVNPKPKEWLQAGWDVVRDFDGYSMGRFLREYAE 287

Qy 221 LSPGAVRMIGDLNEQSMYTALESEMIYDQADVNDSVYTHEYETGGSDLILPEAFLSVLDVP 280

Db 288 FSEDAEVRIGTENMTSRHLAFFHSPIGRSDIDPRATYWEIEGGSRMMPETLAKDLRDQ 347

Qy 281 ILLNSKVYKHROSDD-----GVITYQTGNE----SSLMLDSADIVLVTTA 323

Db 348 IVMQMRVWLRLEYYPGDRGHHGELTGPGCPAVAIQTVPEGEPYAATOTWGTGLIAITVTPF 407

Qy 324 KAALFIDDPPLSISKMEALRSVHYDSTSSTKLLTFRDWK----- 363

Db 408 SSURFVTKTPTPSYKKRRAVIETHYDQTAKVLELFSRRWWTEADWKRELDIAQGLYD 467

Qy 364 -----END-----GIR--- 369

Db 468 YYQQWGEDEAALALPQSVRNLPTGLIAGHPVDSEIGEQVEYYRNSELGGVRPAT 527

Qy 370 ---GGKSTTDGPPRYIYPSHSEFTNETIGVLLASYTWSDESULFGASDEELKELARD 426

Db 528 NAYGGGSTTDNPNRMFYPSHVPGTQG-GVLLAAISWSDDAARWDSFDDAERYGALEN 586

Qy 427 LAKIHGEQWIKCTGIV-IVKWMSADPSLGAFALETFPYQHUEYAQELFSSSEGRVHAGEH 485

Db 587 LQSVHGRREVFTYTAGGTQSWLDRPACGEAAVYTPHQMTAFHLDVRPCPVYAGEH 646

Qy 486 TAFPHAWIETSMKSAIRATAININK 509

Db 647 VSLKHAWTEGAVETAVRAIAVNE 670

Qy 371 -----END----- 515

Db 497 TSYNGWQEGALLAATTAVQEMHKFQASSQA 526

## RESULT 6

A12498 L-amino acid oxidase [imported] - *Nostoc* sp. (strain PCC 7120) plasmid pCC7120alphaC;Species: *Nostoc* sp. PCC 7120A;Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120

C;Date: 14-Dec-2001 #text\_change 09-Jul-2004

C;Accession: A12498

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, E.

DNA Res. 8, 205-213, 2001

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: A12498

A;Species: Deinococcus radiodurans

C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C;Accession: A75581

R'White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma

S.; Smith, H.O.; Ventler, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A; Genome: plasmid	Query Match 14.5%; Score 392; DB 2; Length 426;	Db 267 NGHSRNLSSVDFIPWWQSNSNGLYYVDIK-----NPETGLPPTLAE----LAANSSL 314
Best Local Similarity 25.6%; Pred. No. 9 5e-18;	Matches 130; Conservative 72; Mismatches 172; Indels 134; Gaps 13;	Qy 184 DRAIQKVKEEVEANGCKAALEKYDRE-SYKEYLKE-----EGGLSPGAVRMIGDL 232
Matches 130; Conservative		Db 315 --ALTRVSN---NSTSKLSQKVDFLPLPDTKFLKELAEMAQNMFKAHDWLSCGLAGH.PGDQ 368
Qy 11 SVVSVLITLYSYHTVALSKEHLADCLDKYDTLLQTLNGLPHINTSHHVIVGAGMA 70		Qy 233 LNEQSLMYTALSEMMYDQADNDSVT-----YHEVIGSDILLPPEAFSLV 277
Db 35 SMTAAATVSYDHOAQPKSP-----GTLPKPLR---RKVIVYGAGIS 76		Db 369 WSEFGFMVNVLRGSSLNDTAPALTRTGTRCTKGCTFPRRGDAIDGGLNRLPLSFHPLV 428
Qy 71 GLTAAKLQLDAGHTVITILEANDRUGRVETYRNEKEGW-YAEMGAMRISSHHVIVGAGMA 70		Qy 278 DVPILLNSKYKHI---RQSDKGVI---VSYQTGNBESSLMDLSADIYLVLTFTAKALPFD 331
Db 77 GLVAAYELTAVGHDVTLLEASKRIGGRVLTGAFQGEDLLELGARIPSPNQHLLTGYIK 136		Db 429 DNATTINRRLERVAFFDAETOKVTLIHSRSNSYKDSFESS---EHDAVIAAPFSIVKKWRF 484
Qy 130 KLGVEHNNFVMTDDNNTFYLVNGVRERITYVVOENPDLVKYNTSESEKGISADDLDRALK 189		Qy 332 DPPLSISK---MEALRSVHDSSTKILLTFRDKFEE-DGIGIRGGKSIT-DGPS-RYIY 384
Db 137 HFGKLKLSQFAPADGKYLTIKDGR-----Li-----PAKVLFQNQPQI 175		Db 485 SPALDIHTAPTPLANATONLEYTSACKVALERPRTRFEHLPOPQYGSCTSTDPGIGSICV 544
Qy 190 VKEEVEANGCKAALEKYDRE-SYKEYLKEEGGLSPGAVRMIGDLNNEQSLMYTALSEMMYD 249		Qy 385 PSHSFHTNETIGVLLASY---TWSDSLEFLGASDEELKELALDRALKHGEQ-YWDKC 439
Db 176 RPQEIQ-----		Qy 545 PSYNINGTDGPASILASYISGADMGR---WVSTDEEEHVQYLNAMAETHGEELVKEQY 601
Qy 250 QADVNDSVTYHEVTGGSDLLPFAFLSYLDVPIILNSKVKHITROSKDGKVIVSYQTGNESSL 309		Qy 440 TGVIVRK-WSDAPYSLGAFALFTPYQHOLEYAQELFSSEGRVHFAGHTAAPHWETSMK 498
Db 182 -----KLTDGPDLLPKFAQAQALTKEIKLDPVARIVTQVTSNGEVYSCLSGCR---		Db 602 TQFQFNRCWALDPLLEASWASWASPTVGQHELYLPPEYFOTRNNLVFGHENTSYTHAWASALE 661
Qy 310 MDLSADITFVLTFTTAKAALFIDEDDPPLSISKMEALR-SVHYDSTSSTKILLTFRDKFEDDGI 368		Qy 499 SATRAATNI 507
Db 228 -YLGDXVLCPTVPLTVLNVQTPSPSESEEKKOAAAGYNYRAATRCFVKPNRFFERENL 285		Db 662 SGIRGSVQL 670
Qy 369 RGGKSITDGPSSRYIYPPSHSFHTN---ETIGVLLASYTWSDESTLFLGASDEELKELAL 424		RESULT 8
Db 288 NEWGFFDD-----BELWHTTWDRPEKGILHAYLGKEKGLIDGFFGKTOQQKLL 335		Db A87595
Qy 425 RDLAKIHGEQWIDKCTGVIVK---KNSADPYSLGAFALFTPYQHOLEYAQELFSSEGRVH 480		Qy 426 RDLAKIHGEQWIDKCTGVIVK---KNSADPYSLGAFALFTPYQHOLEYAQELFSSEGRVH 480
Db 336 Q-----HWEKLPLGVSNYSVRSYFHSTWDIWSKGGEWAYPTDEQEKLFPELGKSEKGY 390		C;Species: Caulobacter crescentus
Qy 481 PAGEHTAHPHAIJETSMKAIAATANIN 508		C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
Db 391 PAGEHTSKTRGMQLGQALESGLKAQAEITH 418		R;Nierman, W.C.; Reidblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Heidelberg, J.
		B.; Laub, M.T.; DeBoy, R.T.; Durkin, R.J.; Haft, D.H.; Kolon, J.; Ennalaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Fraser, C.M.
		Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001.
		A;Title: Complete Genome Sequence of Caulobacter crescentus.
		A;Reference number: A87249; PMID:21173698; PMID:11259647
		A;Accession: A87595
		A;Status: Preliminary
		A;Molecule type: DNA
		A;Residues: 1-541 <STOP>
		A;Cross-references: UNIPROT:Q9A4N7; GB:AE005673; PIDN:AAK24757.1; GSPDB:G
		C;Genetics:
		A;Gene: CC2793
		Query Match 14.2%; Score 383.5; DB 2; Length 541;
		Best Local Similarity 26.7%; Pred. No. 4.8e-17;
		Mismatches 92; Mismatches 209; Indels 59; Gaps 15;
		Matches 131; Conservative 92;
		Qy 62 VVIVGAGMAGLTAAKLQLDAGHTVITILEANDRVRGVERTYR-----NEKEGW-- 108
		Db 66 VIVLAGAGLAGLILAAELRKAGYKQILEFQNRPGRNWSURGGDSYTELGGATQRVGYAA 125
		Query Match 109 --YAMGAMRIPSSHRIVOMFVKKGIVEMNEFVMTDDNTTFLYLVNGVRERTYVVOENPDPV 166
		Best Local Similarity 26.7%; Pred. No. 4.8e-17;
		Mismatches 92; Mismatches 209; Indels 59; Gaps 15;
		Matches 131; Conservative 92;
		Qy 109 --YAMGAMRIPSSHRIVOMFVKKGIVEMNEFVMTDDNTTFLYLVNGVRERTYVVOENPDPV 166
		Db 126 GNYFNPGPWRIPHAKTLLHYCKQGVALBPFIQNH----SGWHSSCAFGGKPB-V 177
		Qy 167 KYNVSESE-----KGIISADDLDRALQKVKYKEE-YEANGCKAALEYKDYR-----209
		Db 178 RFNAAAADFFCGNIAELLAKSVNAKADDATVLEDERBLLEALKGWMGLDKDYRASLRT 237
		Qy 210 -SVKEVLKEEFGGLSOGA-----VFMIGDLINEQSLMYTALSEM1YDQADVNDSTYHEV 262
		Db 238 SSHRSFKRPQGGGVGQAPISSDDLYSLHDVLDPQ--WVTSMGFFNHEM---QTMFQP 291
		Qy 263 TGGSDLLPEAFLSVLDVPIILNSKVKHROSDKGIVIVSYOTGENESSLMDLSADIVLVTTT 322
		RESULT 7
A38314	L-amino-acid oxidase (EC 1.4.3.2) precursor - Neurospora crassa	
C;Species: Neurospora crassa		
C;Accession: A38314		
C;Status: preliminary		
A;Molecule type: DNA		
A;Residues: 1-655 <NIE>		
C;Keywords: oxidoreductase		
A;Title: Molecular cloning of the L-amino-acid oxidase gene from Neurospora crassa.		
A;Reference number: A38314; MUID:91009158; PMID:2145270		
C;Accession: A38314		
A;Status: preliminary		
A;Molecule type: DNA		
A;Residues: 1-655 <NIE>		
C;Keywords: oxidoreductase		
Query Match 14.5%; Score 392; DB 2; Length 695;		
Best Local Similarity 27.0%; Pred. No. 2e-17;		
Matches 148; Conservative 90; Mismatches 195; Indels 116; Gaps 26;		
Qy 37 LEDKDYDTLLQTLQDNGLPHINTSHVIVYVGAGMAGLTAAKLQLDAGHT-VTILEANDRVG 95		Db 109 --YAMGAMRIPSSHRIVOMFVKKGIVEMNEFVMTDDNTTFLYLVNGVRERTYVVOENPDPV 166
Db 160 LBDKE---ISTVD---VEAKSKSKNIAIVGACMSGMLTYLCITQAGMTVSIIECGNRG 212		Qy 167 KYNVSESE-----KGIISADDLDRALQKVKYKEE-YEANGCKAALEYKDYR-----209
Qy 96 CRVET-----YRNKEGYWAENGMARIP-----SSHRIV-----SSHRIV-----124		Db 178 RFNAAAADFFCGNIAELLAKSVNAKADDATVLEDERBLLEALKGWMGLDKDYRASLRT 237
Db 213 CRVTEYLSGGCPFDYS-----YQENGMPRFENTITLGNETYVNSDQHQLYFQLAEMNSL 266		Qy 210 -SVKEVLKEEFGGLSOGA-----VFMIGDLINEQSLMYTALSEM1YDQADVNDSTYHEV 262
Qy 125 QMFVKLUGVEMNEFVMTDDNTFYLVNGVRERTYVVOENPDY-LKTNVSESEKGISADDLL 183		Db 238 SSHRSFKRPQGGGVGQAPISSDDLYSLHDVLDPQ--WVTSMGFFNHEM---QTMFQP 291



Proc. Natl. Acad. Sci. U.S.A. 82, 6522-6526, 1985  
 A;Title: Nucleotide sequences of the *Pseudomonas savastanoi* indoleacetic acid genes show  
 A;Reference number: A94062  
 A;Accession: A25493  
 A;Molecule type: DNA  
 A;Residues: 1-557 <PDB>  
 A;Cross-references: UNIPROT:P06617  
 C;Genetics  
 A;Gene: IAM  
 C;Superfamily: Pseudomonas tryptophan 2-monoxygenase  
 C;Keywords: monooxygenase; oxidoreductase

Query Match 11.2% Score 302; DB 1; Length 557;  
 Best Local Similarity 24.8%; Pred. No. 9e-12;  
 Matches 129; Conservative 83; Mismatches 202; Indels 106; Gaps 18;

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  Qy 62 VVINGAGMAGITAAKLQDAG-HTYTILEANDRYGGRV-EYTRNEKGWYAEMGANRIP 118
  Db 41 VAIRVGAGISGLVAATTEBLRAGVKDQVLYESDRIGGRWSQFDQTTRRYIAEMGANRFP 100
  Qy 119 SSHRIVQWFWYKKGVMNEPV---MTIDNTFYLVNGTRTYVVOENPDVKYNNVSE 174
  Db 101 PSATGFHYLKKFGF1STTFPDGCVDTBLYH-RGGRYHWAGKRPPELFRRTBGWQ 158
  Qy 175 KGISADDLLRALOKVKEEVEANGCKAAALKV----- 206
  Db 159 SLLSGGYLLEGGSLVAPLDTAMLKSGRBEAAIAWQCFWNLVERDCSFYNAIVCIFGRH 218
  Qy 207 ---DRYSVKEYLKEEGGLSPGAIVRMICDLINEOSIMYTALESIMYD-QADVNDSVTYH 260
  Db 219 PPGGDRWRAPPEDFELFGSLGIGS---GGFLPVFOAGTEILRMVINGYQSD----- 266
  Qy 261 EVTGGSDLIPEAFASV-----LDVPLLN---SKVKHRIQSDKGKVIVSYQTGNESS 308
  Db 267 -----QRLTPDGSSLAAARLADQSFDGKALDRVCFSRVRGVSREAAKIIQTEADEQRV 321
  Qy 309 LMDLSADTVLVTITKAALFI----DEPPDLTSKMEALRSYHDSSKILLTFRDKFW 364
  Db 322 F-----DRVITVSSNRAQMOMIHCGLTDSSSELSFSDVARAVREFHTLGSSKLFILTTRKFW 375
  Qy 365 DDGIRGGKSIT--DGPSRYTYPSPHSPTNETIGVLLAYSTWSDSLSLFLGASDEELK- 420
  Db 376 --TKNKLPTTQSDFGLRGVCLDYQDDEPBGHGVWLSTSWEADAQKMLAMPDKTRC 432
  Qy 421 ELALRDIAKIHGEQV-----WDKCTGIVVKKWSDAPSISGAFALFTPYOHLTEAQELF 473
  Db 433 QVLYDDLAIAHPTPASYLVPDODCYERYVLHHDWLDPHSAGFKLNYPGEDV-TSQLRF 491
  Qy 474 -----SSEGRRVHPAGEHTAPPHMIEFTSMKSAIRAA 504
  Db 492 FQPMTANSNPKDGTGLYLAGCSCSFAGGWIEGAVOTALNSA 531
  
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RESULT 12

JH0817  
 A;Alternate names: monamine oxidase B  
 C;Species: Homo sapiens (man)  
 C;Date: 30-Sep-1993 #Sequence\_revision 20-Aug-1994 #text\_change 09-Jul-2004  
 C;Accession: JH0817; JH0818; B16175; S66431  
 R;Chen, K.; Wu, H. F.; Shih, J. C.  
 J;Neurochem. 61, 187-190, 1993  
 A;Article: The deduced amino acid sequences of human platelet and frontal cortex monoamine oxidase (flavin-containing) (BC 1.4.3.4) B - human  
 A;Reference number: JH0817; MUID:93294532; PMID:6515265  
 A;Accession: JH0817  
 A;Molecule type: mRNA  
 A;Residues: 1-520 <PDB>  
 A;Cross-references: UNIPROT:P27338; GB:S62734; NID:9398414; PIDN:ABA27229.1; PID:9398415  
 A;Experimental source: platelet  
 A;Accession: JH0818  
 A;Molecule type: mRNA  
 A;Residues: 1-520 <CH1>  
 A;Cross-references: GB:S62734; NID:9398414; PIDN:ABA27229.1; PID:9398415  
 Db 369 AKVLGSLDEALEPVPHYEE-----KNWCEQYSGGCYTYFPPIGLTQYGRVLRQPV 418

A;Experimental source: cerebral cortex  
 R;Bach, A.W.J.; Lan, N.C.; Johnson, D.L.; Abell, C.W.; Bembenek, M.E.; Kwan, S.W.; Seebu  
 Proc. Natl. Acad. Sci. U.S.A. 85, 4934-4938, 1988  
 A;Title: cDNA cloning of human liver monoamine oxidase A and B: molecular basis of difference  
 A;Reference number: A36175; MUID:88263063; PMID:3387449  
 A;Accession: B36175  
 A;Molecule type: mRNA  
 A;Residues: 1-520 <PDB>  
 A;Cross-references: GB:M6135; GB:I03793; NID:9187374; PIDN:AAA9551.1; PID:9187376  
 A;Experimental source: tissue liver  
 A;Note: parts of this sequence were determined by protein sequencing  
 R;Zhu, Q.S.; Grimsby, J.; Chen, K.; Shih, J.C.  
 J;Neurosci. 12, 4431-4446, 1992  
 A;Title: Promoter organization and activity of human monoamine oxidase (MAO) A and B genes  
 A;Reference number: I41054; MUID:93057796; PMID:432104  
 A;Accession: I62455  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Residues: 1-15 <PDB>  
 A;Cross-references: GB:M89637; NID:9187378; PIDN:AAB46386.1; PID:9553527  
 A;Experimental source: cell-line 1635  
 R;Cesura, A.M.; Gottowik, J.; Lahn, H.W.; Lang, G.; Imhof, R.; Malherbe, P.; Roethlisberger, J.; Bloch, 236, 996-1002, 1996  
 A;Title: Investigation on the structure of the active site of monoamine oxidase-B by aff  
 A;Reference number: S66431; MUID:96270755; PMID:8665924  
 A;Molecule type: protein  
 A;Residues: 371-391 <CBS>  
 C;Genetics:  
 A;Gene: GDB:MAOB  
 A;Cross-references: GDB:119377; OMIM:309860  
 A;Map position: xp1.23-xp1.23  
 C;Function:  
 A;Description: catalyzes the oxidative deamination of many neuro-transmitters and dietary  
 F:6-34/Region: beta-alpha-beta-protein; oxidoreductase; phosphoprotein  
 E:397/Modified site: S-(8alpha-FAD)-cysteine (Cys) #status predicted  
 Query Match 10.7% Score 288; DB 2; Length 520;  
 Best Local Similarity 25.0%; Pred. No. 6.5e-11; Gaps 27;  
 Matches 13; Conservative 84; Mismatches 169; Indels 140; Gaps 27;  
 Qy 62 VVIVAGMAGLTAALKLQDAGHTVTLANDRVGRVETYNEKEGVWAEMGMARI-PSS 120
 Db 7 VVVGGGSGMAAKLQLDGSVNVVLEARDRGGRVYTLLRKVQ-K-YVDLGGSYvPTQ 65
 Qy 121 HRIVQFWVKKLGVE---MNEFMTDDNTFYLGVERTYVQE---NPDVLYKVNVS 171
 Db 66 NRILR-LAKELGLETYKNEVER----LTHHVKGKSYPPRGPPPPVWNP-ITVY--- 112
 Qy 172 ESEKGISADDLL----RALOKVKEEVEANG-CKAAL-EKYDRYSYKEVKEEGGLSPG 224
 Db 113 -----LDHNMFRTMDMGREPSDAWPKAIAEEDNMNTMKELL----- 152
 Qy 225 AVRIGDGLNEQSLIMYTALESIMYDQADVNDSVT-YHEVT----- 263
 Db 153 -----DLCLWATESAKAALFDFDPLSISKMEALRSVHYDSSTKILLTRDKFEDDGIRGGK 372
 Qy 264 -----GGSDLLPDEAFLSVLDPVILLNSKVKHIRDQSKGIVVSYQTGNESSLMDL 312
 Db 201 TTNGGQERKFKVGGSGQSERIDLQGDRVKLERPVYIDQPRENVLY-ETLNHEM--Y 255
 Qy 313 SADIVLVTTAKAALFDFDPLSISKMEALRSVHYDSSTKILLTRDKFEDDGIRGGK 372
 Db 256 EAKVVISAIPTLGMKIHNPPLMMRNQMTRPVGSVRCIVYYKEPFKRDY-CGT 314
 Qy 373 SITDQPSRYIY-----PSHSFHTNETIGVLLASTWSDESLLFLGASDEELKEU---- 422
 Db 315 MIDGEAPVAYLDDTKPEGNYAA-IMGFILAHKARKLARL--TKEERLKKLCELY 368
 Qy 423 -----ALRDLAKIHGQWWDKCTGVIVKWKNSADPSIGAFALEPTPYOHL-BYAQEFLPSSE 476
 Db 369 AKVLGSLDEALEPVPHYEE-----KNWCEQYSGGCYTYFPPIGLTQYGRVLRQPV 418

C:Date: 24-Mar-1999 #Sequence\_revision 24-Mar-1999 #text\_change 09-Jul-2004  
 C:Accession: T03187 R:Tavadorai, P.: Schinina, M.; Cecconi, F.; Di Agostino, S.; Manera, F.; Rea, G.; Mar  
 FBES Lett. 426, 62-66, 1998  
 A:Title: Maize polyamine oxidase: primary structure from protein and cDNA sequencing.  
 A:Reference number: 214918; MUID: 98258926; PMID: 9598979  
 A:Accession: T03187  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-500 <TA>  
 A:Cross-references: UNIPROT: 064411; EMBL: AJ002204; NID: g3043528; PIDN: CAA052491; PID: 9  
 A:Experimental source: cultivar Paolo  
 A:Note: flavin-containing protein  
 C:Genetics:  
 A:Gene: PAO  
 A:Genome: plasmid PCR2.1  
 C:Keywords: oxidoreductase  
 Query Match Score 285.5; DB 2; Length 500;  
 Best Local Similarity 25.8%; Pred. No. 8.9e-11;  
 Matches 141; Conservative 91; Mismatches 221; Indels 93; Gaps 25;  
 Qy 10 LSYVSVLITLYSHTVALSKHADLEDKDYDTLLQTDLNGLPHNTSHHIVVAGAGM 69  
 Db 10 LAVAALL-----ALSAQH-----GSLAATVGPRVIVVGAGM 42  
 Qy 70 AGTTAAKILODAHT-YTILEANDRYGGRVETYRNKEGYAEMGMARIPSSHRIVQMFV 128  
 Db 43 SGISAAKRLSEAGITDILLEATDHIGRM-HKTNPAGINELGA-----NWVE 90  
 Qy 129 KKLGVEMNEFWMTDDNTFYLNVGRERTYVQENPDVLYKVNSESEKGISADDLDRALQ 188  
 Db 91 GYNGKGNPWPINVSPLKLN-----PRSFSDYLAQNYKEDGVYDYYQKRIE 142  
 Qy 189 KVKEVEANGCKAALEKY---DRYSV-KRVLKEBEGGLSPGA-VRMIGD----- 231  
 Db 143 -LADSVEEMGBLSATHASGRDDMSILAMQRLNHEOPNGPATPDMVDDYKFDEYFAE 201  
 Db 232 ----LLNEBSOL-MYTALSEMIDQADVN--DSTVYHEVTGSDILPEAFSLVDYPL 282  
 Qy 202 PPRVTSLOQNTVPLATPSDFGDDVYFYADQRGYEAVVYY-LAQYQLKTDKSKVIVDPLQ 260  
 Db 283 LNSKVKHIIROSDFDGIVVSYQTGNESSUMDL&ADIVLYTT--AKAALFIDFDPPSLSKM 340  
 Db 261 LNKVRBIKVSFGGTIVKTE--DNEV--VSADYNNVASLGVLODQIOPKPKLPTWKV 315  
 Qy 341 BALRSVHYDSSTKLLTPDKFEDDGIRGOKSITDGPSTVYIYPSHSFTHNE-TIGVL 398  
 Db 316 RAIYQFDMAVYTTFKPKRFWPWEG-KGREFFLYASSRGRGYGQWEPEKQYPDANVL 373  
 Qy 399 LASYTMWSDESLFLGASDEELKELALRDLALKH-GEQWWDKCTGVTKWNSADPYSLGAF 457  
 Db 374 LVTVT-DEESRIERIOQSDEQTKAEMQVLRKMPGKDVPD-ATDILVPRWSDRFPKGTF 431  
 Qy 458 ALP-TPYQHLEYAQOLFSSSEGRVHAGEHTA-FPHAWIETSMKSRAATANTINKYANNEES 515  
 Db 432 SNWPGSVNRYEQDO-LRAPPVGRVYTFGEHTSEHYNCVHGAFLSGIDSAAELTLNCQKKM 490  
 Qy 516 TIEHTK 521  
 Db 491 CKYHVQ 496  
 RESULT 15  
 A36175  
 amine oxidase (flavin-containing) (EC 1.4.3.4) A - human  
 N:Alternate names: adrenalin oxidase A; amine oxidase A; monoamine oxidase A; tyraminase  
 C:Species: Homo sapiens (man)  
 C:Accession: A36175; JL0066; R28935; 184543; S23160  
 C:Date: 14-Dec-1990 #Sequence revision 14-Dec-1990 #text\_change 09-Jul-2004  
 T03387  
 T03387  
 polyanine oxidase (EC 1.5.3.11) precursor - maize plasmid PCR2.1  
 C:Species: Zea mays (maize)

A;Reference number: A36175; MUID:88263063; PMID:3387449	Db	161 IDKICWTKTA-RRFAYLFVNINVTSEPEVSAWMFLWYVKOCGGTRIFSVTNGGOERKF 219
A;Molecule type: mRNA	Qy	264 -GGSDLIPPEAFLSVLDPVILNSKVKHROSDFKGIVIVSQTGNEESSMLDSADIIVLTFT 322
* A;Residues: 1-527 <BAC>	Db	220 VGGSGOYSERIMDLIGDQVQLNHPTVHDOSSDNIIIE-TLNHEYECKVTVNAAPPTLT 278
A;Cross-references: UNIPROT:P21397; GB:J03792; NID:9187352; PID:9187353	Qy	323 AKAAFLPIDEFPPLTSKMEALRSVYHDSSTSPTKILLTFRDKFWEDDGIRGGKSITDGPSPRYI 382
A;Experimental source: brain frontal cortex; liver; Placenta	Db	279 AK---TINFRELPERNQLQIQRPMGAVTKCMYMYKEAWKKKDYCGMTIEDDAPI- 333
A;Note: parts of this sequence were determined by protein sequencing; the amino end of R HSU, Y.P.; Weyler, W.; Chen, S.; Sims, K.B.; Rinehart, W.B.; Utterback, M.C.; Powell J. Neurochem. 51, 1321-1324, 1988	Qy	383 YPPSISFHTNST-----IGVLLASYTWSDESLFLGASDEELKELAIRD-LAKIHG 432
A;Title: Structural features of human monoamine oxidase A elucidated from cDNA and peptide	Db	334 ----SITLDDTKPDGSLLPAIMGFLLARK-ADR---LAKLHKIRKKKICELAKVLG 382
A;Accession number: JL0066	Qy	433 EQVWDKCTGVVKKNSADPSIGAF-ALIFTPYQHLEYAQEFLSSGRVHFAGEMTA---- 487
A;Molecule type: mRNA	Db	383 SQEALHPVYEEBKNCREEQYSGGCYTAYPPGIMMQYGRVIROPVGRIFFAGETATKWS 442
A;Residues: 1-527 <HSU>	Qy	488 -FPHAWIETSMKSARAATATINKVANEESTEHTKDE 523
A;Cross-references: GB:M692226; NID:9187354; PID:9187355	Db	443 GYMEGAEVAGERAAREVNLGIGKVTEKDIAWQEPBSK 479
A;Experimental source: liver	Qy	443 GYMEGAEVAGERAAREVNLGIGKVTEKDIAWQEPBSK 479
R.Zhu, Q.S.; Grimsby, J.; Chen, K.; Shih, J.C.	Db	Search completed: October 4, 2005, 14:04:27
J. Neurosci. 12, 4437-4446, 1992	Job time : 47 secs	
A;Title: Promoter organization and activity of human monoamine oxidase (MAO) A and B gene	Qy	
A;Reference number: A30150; MUID:89025882; PMID:3178846	Db	
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A;Residues: 31-45;62-79;110-129;268-288;298-316;319-332;336-352;372-396,'M',398-412;430-	Qy	
A;Experimental source: placenta	Db	
R.Chen, Z.Y.; Horamishigil, G.S.; Huang, J.K.; Wen, L.; Ezzedine, D.; Aydin-Muderisoglu	Qy	
Nucleic Acids Res. 19, 4537-4541, 1991	Db	
A;Title: Structure of the human gene for monoamine oxidase type A.	Qy	
A;Reference number: S23360; MUID:91360358; PMID:1886775	Db	
A;Accession: S23360	Qy	
A;Status: nucleic acid sequence not shown; translation not shown	Db	
A;Residues: 1-24 <RES>	Qy	
A;Cross-references: GB:9187356; PIDN:ABA46385.1; PID:9553526	Db	
R.Chen, Z.Y.; Horamishigil, G.S.; Huang, J.K.; Wen, L.; Ezzedine, D.; Aydin-Muderisoglu	Qy	
Nucleic Acids Res. 19, 4537-4541, 1991	Db	
A;Title: Structure of the human gene for monoamine oxidase type A.	Qy	
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A;Accession: S23360	Qy	
A;Status: nucleic acid sequence not shown; translation not shown	Db	
A;Residues: 1-102;138-527 <CHW>	Qy	
A;Cross-references: EMBL:Xe0818	Db	
A;Note: the nucleotide sequence was submitted to the EMBL Data Library; July 1991	Qy	
C;Comment: This protein is an integral protein of the outer mitochondrial membrane and is	Db	
C;Genetics:	Qy	
A;Gene: GDB:MAOA	Db	
A;Cross-references: GDB:120164; OMIM:309850	Qy	
A;Map-position: Xp11.23-Xp11.23	Db	
C;Complex: dimer	Qy	
C;Function:	Db	
A;Description: catalyzes the oxidative deamination of dietary amines and neurotransmitter	Qy	
F15-13/Region: beta-alpha-beta FAD nucleotide-binding fold	Db	
F1406/Modified site: S-(8alpha-FAD)-cysteine (Cys) #status predicted	Qy	
Query Match Score 10.5%; Length 527;	Db	
Best Local Similarity 23.4%; Pred. No. 1.4e-10; Gaps 18;	Qy	
Matches 121; Conservative 91; Mismatches 197; Indels 108; Gaps 18;	Db	
Qy 62 VVIVGAGAGLPAKLIQDAQHTVTVLLEANDRGGRTVETTYVQE-----NP-DVLYKVNVESE 121	Db	
Db 76 RLRL-LSYGLGETYKVNSE---RLVQYVKGKTPFRGAPPVWNPIAYLDN---- 125	Qy	
Qy 175 KGISADDLDRALQKVKBEVEANGCKAA--LEKYDRYSVKYLKEEGGLSPGAVRMIDL 232	Db	
Db 126 -----NLWRTIDNMGRKEIPTDAPWQAQHADWKDRMTMK-----L 160	Qy	
Qy 233 LNEQSILMVNTALSEMIYDOADYNDSDVTHVET----- 263	Db	